OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.7
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Run on: February 21, 2006, 13:13:43 ; Search time 259 Seconds
5497.401 Million cell updates/sec
(without alignments)

Title: US-10-600-070B-2
Perfect score: 4063
Sequence: 1 MEALSHVGIGLSPFQLCRLP.........YEVFWSKSGWKITEGSVLAS 801

Scoring table: BLOSUM62
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Ygapop 10.0 : Ygapext 0.5
Fgapop 6.0 : Fgapext 7.0
Delop   6.0 : Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Database : Issued_Patents_NA:*
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SUMMARIES

Result No.	Score	% Query Match	Length DB	DB ID		Description
1	148.5	3.7	6270	2	US-08-418-893D-25	Sequence 25, Appl
2	140	3.4	2668	2	US-08-461-775-11	Sequence 11, Appl
3	140	3.4	2668	3	US-09-031-606-11	Sequence 11, Appl
4	140	3.4	2969	3	US-09-057-969-1	Sequence 1, Appli
5	139	3.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
6	139	3.4	2631	2	US-08-436-664-33	Sequence 33, Appl
7	136.5	3.4	2631	3	US-08-135-642-33	Sequence 33, Appl
8	136.5	3.4	2631	3	US-08-394-232A-33	Sequence 33, Appl
9	136.5	3.4	2631	6	PCT-US95-04080-33	Sequence 33, Appl
10	134.5	3.3	2631	2	US-08-436-664-21	Sequence 21, Appl
11	134.5	3.3	2631	2	US-08-436-664-31	Sequence 31, Appl
12	134.5	3.3	2631	3	US-09-135-642-21	Sequence 21, Appl
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16	134.5	3.3	2631	6	PCT-US95-04080-21	Sequence 21, Appl
17	134.5	3.3	2631	6	PCT-US95-04080-31	Sequence 31, Appl
18	134.5	3.3	2761	2	PCT-US95-04080-19	Sequence 19, Appl
19	134.5	3.3	2761	3	US-08-394-232A-19	Sequence 19, Appl
20	134.5	3.3	2761	6	US-09-135-642-19	Sequence 19, Appl
21	134	3.3	2761	6	US-08-436-664-19	Sequence 19, Appl
22	134	3.3	2761	2	PCT-US95-04080-3	Sequence 3, Appli
23	134	3.3	33529	2	US-09-144-085-3	Sequence 3, Appli
24	133.5	3.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
25	132	3.2	3783	3	US-09-902-016-2647	Sequence 2647, Ap
26	131.5	3.2	5588	2	US-09-540-621	Sequence 621, Appl
27	131.5	3.2	3585	2	US-08-680-326-28	Sequence 28, Appl
28	131.5	3.2	124884	3	US-09-661-596A-76	Sequence 76, Appli
29	131.5	3.2	124884	3	US-09-913-514-1	Sequence 1, Appli
30	129.5	3.2	124884	3	US-10-288-823-76	Sequence 76, Appli
31	128.5	3.2	2715	3	US-09-712-363-101	Sequence 101, App
32	128.5	3.2	6790	2	US-08-418-893D-22	Sequence 22, Appl
33	127.5	3.1	125157	3	US-09-913-514-2	Sequence 2, Appl
34	126.5	3.1	3162	3	US-09-252-991A-8094	Sequence 8094, Ap
35	126.5	3.1	7419	3	US-09-252-991A-481	Sequence 481, App
36	126	3.1	7449	3	US-09-252-991A-396	Sequence 396, Appl
37	126	3.1	77536	3	US-09-410-551B-1	Sequence 1, Appli
38	125.5	3.1	77536	3	US-09-252-991A-727	Sequence 727, App
39	125.5	3.1	19068	3	US-09-902-540-1123	Sequence 1123, Ap
40	124.5	3.1	31063	3	US-09-596-002-20	Sequence 20, Appl
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43	123.5	3.0	1664976	3	US-08-692-570-1	Sequence 1, Appl
44	123.5	3.0	1664976	3	US-09-692-570-1	Sequence 1, Appl
45	123	3.0	2496	2	US-08-073-384C-2	Sequence 2, Appl

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-08-418-893D-25
Sequence 25, Application US/08418893D
Patent No. 5559220
GENERAL INFORMATION:
APPLICANT: ROESSLER, PAUL G
APPLICANT: OHLROGGE, JOHN B
TITLE OF INVENTION: GENE THAT ENCODES ACETYL-COENZYME A
TITLE OF INVENTION: CARBOXYLASE FROM CYCLOTELLA CRYPTICA
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NATIONAL RENEWABLE ENERGY LABORATORY
STREET: 1617 Cole Blvd.
CITY: Golden
STATE: CO
COUNTRY: USA
ZIP: 80401-3393
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,893D
FILING DATE: April 7, 1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,938
FILING DATE: September 14, 1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: O'CONNOR, EDNA
REGISTRATION NUMBER: 29,252

REFERENCE/DOCKET NUMBER: MRI/NREL IR# 92-48CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-231-1000
TELEFAX: 303-231-1098
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
  LENGTH: 6270 bases
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: DNA
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
US-08-418-893D-25

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
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US-10-600-070B-2 (1-801) x US-08-418-893D-25 (1-6270)

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	148.50
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Conservative:	119
Mismatches:	305
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Gaps:	48

Percent Similarity: 33.3%
Best Local Similarity: 20.3%
Query Match: 3.7%

(sequence alignment data in image)

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; TITLE OF INVENTION:   REGULATORY NUCLEOTIDE SEQUENCE OF THE
; APPLICANT:            Gerard
; APPLICANT:            GUGLIEMI, Philippe
; APPLICANT:            MAZODIER,
; GENERAL INFORMATION:
; Patent No. 5858773
; Sequence 11, Application US/08461775
US-08-461-775-11
RESULT 2
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NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
   ADDRESSEE:  Burns, Doane, Swecker & Mathis
   STREET:     George Mason Bldg., Washington & Prince Sts.
   CITY:       Alexandria
   STATE:      Virginia
   COUNTRY:    United States
   ZIP:        22313-1404
COMPUTER READABLE FORM:
   MEDIUM TYPE:   Floppy disk
   COMPUTER:      IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:    PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/08/461,775
   FILING DATE:
   CLASSIFICATION:  435
PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  US 08/050,313
   FILING DATE:   10-MAY-1993
   APPLICATION NUMBER:  FR 9011186
   FILING DATE:   10-SEP-1990
ATTORNEY/AGENT INFORMATION:
   NAME:  Crane-Feury, Sharon E
   REGISTRATION NUMBER:  36,113
   REFERENCE/DOCKET NUMBER:  010830-035
TELECOMMUNICATION INFORMATION:
   TELEPHONE:  (703) 836-6620
   TELEFAX:   (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
   LENGTH:  2668 base pairs
   TYPE:   nucleic acid
   STRANDEDNESS:  single
   TOPOLOGY:  linear
   MOLECULE TYPE:  DNA (genomic)
US-08-461-775-11
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Pred. No.:                      7.95e-05
Score:                         140.00
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Db 2284 CCCTATCTCGAGGTTGAAGGCGATGAAGATGATC------------------ATGCCAATCAAGGCTACTGAG 2337

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Qy  642 SerSerPheGlnArgLysAspMetValSerSerMetGlu---SerAspValAlaThrIle 660
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Db 2431 AAGAAAATAGAAACTTTTTCGGGCAAATTGACATTATTGGAATCGAAGGTTGACTTAGAA 2490

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Qy   145  SerArg----------ArgGluTyrAsnGluGlyLeuLeuAspAspGluGluAla  159
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Qy   160  ThrValIleThrAspVal----------ProTrpAspLysValProGlyAlaLeuCys  175
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Qy   199  ProLysSerPheLysGlnAspVal----------ValLeuValMetAlaLeuAlaPheLeu  215
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Db  1128  CTG-------GCCCAGGGCGCTGGTCCGCGCAACCTGCGGGGC  1181

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Db   216  AspValSerArgAsp-----------AlaMetAlaLeuAspPro  226

Qy   227  ProAspPheIleThrGlyTyrGluPheValGluValLysLeuLeuGlnGlu  246
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Db  1242  GACACCGCCGGATCGACAAGTCCGACATCGCCGGCGGCTTCCGCG  1301

Qy  1302  CAGGACAAGCAGGTCGGC---GAGCTCATCGCCGAGGCCGGATGGACAAGGTCGGCAAGGAC  1358
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Db   247  GlyAlaSerSerLeuIleAlaProAspLeuArgAlaGlnIleAspGluThrLeuGluGlu--  265

Qy   266  ----------------IleThrProArgTyrValLeu------GluLeuLeuGly  276
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Db  1359  GGTGTCATCACGTCGGAGGTCCAACACCTTCGGGTTCTCGACCTGACTTCACCGAGGGC  1418

Qy  1419  ATGGCCTTCGACAAGGGCTACTCTGTCCCGTACATTGTGACCGGCTATGGAC  1478
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Db   277  LeuProLeuGlyLysAspTyrAlaAlaLysAsnGlyLeuSerGlyValArgAsn  296

Qy   297  IleLeu-----------------------------GluLeu  298
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Db  1479  GCCGGTCCTCGACGACCCGTACAATCCTCGATCAGGGCCAAGATCGGTTCGGATCCAGGAC  1538

Qy  1539  CTGCTCGCCGCGTCGGAGAAGGTCATCCAAGGCGGGGTGGCTCCAAGCCGCTGCTGATCATC  1598
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Db   299  ---TrpSerValGlyGlyGlyValAlaSerAlaLeuValGlyGlyLeuThrArgGluLys  317

Qy   318  PheMetAsnGluAla-----------PheLeuArgMetThrArgLeuAlaGlyLeuAla  332
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Db  1599  GCCGAGGACGGTCGACCAGGCGGAGCGCCCTGGTTGCTGCAAGATCCGGCGCCACG  1658

Qy  1659  TTCAACGGCGTGCCGGTCAAGGGCCCGGCCGGCCCGGTGACCGGCGGATCGTCGGC  1718
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Db   333  AspLeuPheValAlaAlaThrProSerAsnIleProAlaGluSerPheGluValTyrGlyGlu  352

Qy   353  AlaLeuAlaLeu-----------ValAlaGlnAlaPheIle  362
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Db  1719  GACACTGGCCACCCTCACCGGGTCCACGGCTCATCGCCGAG  1763

Qy  1764  GGCCTCAAGCTCGACCAGGCCGTCGGACGGTGCTGGGCCACCCGGGCGTCGGCCCGT  1823
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Db   363  GlyLysLysProHisLeuLeuGlnAspAlaAspLysLysGlnIleGlnLeuGlnHisAla  382

Qy   383  LysValMetAlaMetGluIleProAlaMetLeuTyrAspThrArgAsnAsnTrpGluIle  402
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Db  1824  ACCAAGACGACGACCATCGTTGGACGAGAAGCAACGCCGAGGAGGTTCCAGGGC---  1880

Qy  1881  -----CGCGTCGCCCAGATCAAGGCCGACCTCGACCGACTCGGACTGGGGACCGC  1934
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Db   403  AspProPheGlyLeuGluArg-----------GlyLeuCysAlaLeuLeuIleGly  416

Qy  1935  GAGAAGCTTCCAGGAGCGCTCGGCCAAGCGTCGGCGTGATCCGCGTCGGC  1994
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Db   417  LysValAspGluCysAsrgMetTrpLeuGlyLeuAspSerGluGlnTyrArg--  435

Qy   436  -------------------AsnProAlaIleValGluPheValLeuAsnSerAsn  448
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Db   455  LeuProGlyLeuCysLysLeuLeuGluThr-----------------TrpLeuAla---  467

Qy   468  -------------------GlyValValPheProArgPheArgAspAspLysLysPhe  482
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Db  2157  GCCACCCGTGTCGCGGTGCGGTCCGCGGCGGTCTGCGCCGCTGGAAGCCCGGCCAG  2216

Qy  2217  AACGCCGGGCCTCGAGGGGCTACGTCATC-----ACCACCAAGGTGGGGAGCTC  2264
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Db   483  LysLeuGlyLysAsp-------------------TyrTyrTyrAspAspProMetValLeuSer  495

Qy   496  TyrLeuGluArgValGluValGlnGlyLysSerProLeuAlaAlaLeuAlaAlaThrMetAla  515
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Db  2265  GACAAGGGCCCAGGGCTTCAAGCGGGGAGCCACCGGGTACGGCCCGGCGGCCGGC  2324

Qy  2325  GTCATCGACCCGGTCAAGGTCACCGGC---TCCGCCCTTGGAGAACGCCGTCCATCGCC  2381
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Db   516  ArgIleGlyAlaGluHisValLysValAlaSerAlaMetGlnAlaLeuGluGlnLysAsrVal-PhePr  535

Qy   536  ------------------------TCCCTGCTTCCTCCGACGGACGAGACCTGGTC  2411
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Db  2382  ----------------------------------------------------------  

Qy  2412  GTCGGAGAAGCCCGCCCGAGGAGGGCCGGGGGCACCACCAGCCACTGA  2471
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Db   535  oSerArgTyrArgAspArgAsnSerAlaGluProLysAspValGlnGluThrValPhePhe  555

Qy   555  rValAspProValGlyAspAsnAsn-----------ValGlyArgAspGlyGluProGlyVal  571
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Db  2472  GGCTGACCCCTTCCGCAGCCGACGGACCCGGCGCCCGGTCGGCGGCCGGGGGGGCTC  2526
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```
ATTORNEY/AGENT INFORMATION:
   NAME: Crane-Feury, Sharon E
   REGISTRATION NUMBER: 36,113
   REFERENCE/DOCKET NUMBER: 010830-035
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (703) 836-6620
      TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 2668 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
   MOLECULE TYPE: DNA (genomic)

US-09-031-606-11

Alignment Scores:
   Pred. No.:
   Score:                        7.95e-05
                                 140.00
   Percent Similarity:           35.1%          Length:        2668
   Best Local Similarity:        19.9%          Matches:        139
   Query Match:                  3.4%           Conservative:   106
   DB:                                          Mismatches:     255
                                                Indels:         199
                                                Gaps:            34

US-10-600-070B-2 (1-801) x US-09-031-606-11 (1-2668)
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Qy   27 ArgArgSerHisAsnThrSerThrThrIleCysSerAlaSerLysTrpAlaAspArgLeu    46
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Qy   47 LeuSerAspPheAsnPheThrSerAspSerSerSerSerPheAlaThrAlaThrThr       66
Db  627 AGTACAACGGCGAGGAGTACCTGTCCTCTCCGACCGTTCTCCCCATCATCGAGA         686

Qy   67 ThrAlaThrLeuValSerLeuProProSerIleAlaAspArg---ProGluArgHisValPro  85
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Db  687 AGT----------------AGCAGGCCGGACGCGGTCCGGACGGGCAGAGACTTCA       734

Qy   86 --------------IleProIleAspPheTyrGlnValLeuGlyAlaGln              97
Db  735 CCTTTTTCCTGAAGCGCCCCCCTGGGCAGTCGTTTGCCGGTGGCGGAGGGGGG          794

Qy   98 ThrHisPhe------------LeuThrAspGlyIleLeuArgArgAlaAlaPheGluAla    111
          |||
Db  795 TTTCATTTCGAGAGGCGCGGCGGCGGCAGGCCGCTCCGAGACGGATTCGAAAAGCTCCCATGGCG  854

Qy  112 ArgValSerLysProProGlnPheGlyPheSerAspAspAlaLeuLeuIleSerArgArgGln 131
Db  855 AAGATTCTGAAG----TTCGACGAGACGCC--CGTTCGC                        887

Qy  132 IleLeuGlnIleAlaAlaCysGluThrLeuSerAsn-------ProArg             144
          ||||                              |||
Db  888 GCCCTTGAGCGCGGCGGGTGAAACCAGCTGCGCCGACACCGTCAAGGTGACCATCGGCCCCAG  947

Qy  145 SerArg-----------ArgGluTyrAsnGluGlyLeuLeuAspAspProGluGluAla    159
          :::           |||
Db  948 GGCCGCAACGTCGTCGACAAGAAGTTCGGCGCCCGACCATCACCAACGACGCCGTC      1007

Qy  160 ThrValIleThrAspVal----------ProTrpAspLysValProGlyAlaLeuCys    175
          ||:|:                    |||
Db 1008 ACCATCCCCCGTGAGGTTCGAGTGGCGACGACCGCTACGACGAACCTCGGCGCCCCAGCTCGTC 1067

Qy  176 ------------------ValLeuGlnGluGlyCysGlyGluThrGlyIleVal        186
                            :::
Db 1068 AAGGAGGTGGCGACCAAGACCAACGACATCGGGGTGACGGCCACCACCGGACCGTG      1127

Qy  187 LeuArgValGlyIleValAlaLeuLeuLeuLysGluValGlu-----              198
          |||------                                ::|||
Db 1128 CTG-----GCCCAGGCGCCTGGTCCGCCAACGTCGCCAAGGGCGTCGCCAAGGGCC      1181

Qy  199 ProLysSerPheLysGlnAspVal----------ValLeuValMetAlaLeuAlaPheLeu 215
          |||                    :::      |||
Db 1182 CCGGCCGCGCCCTGAAGAAGGGCATCGAGGCGCGGCGTCGCGGAGCTCGCTC          1241
```

```
Qy  216 AspValSerArgAsp------------------AlaMetAlaLeuAspPro           226
          |||                            |||
Db 1242 GACACCGGCGCGCCCGATCAGACGACAAGTCCGACATCGCGCCGGTCTCCGCG         1301

Qy  227 ProAspPheIleThrGlyTyrGluPheValGluGluIleAlaLeuLeuGlnGluGlu     246
          |||
Db 1302 CAGGACAAGCAGCAGCCGGC---GAGCTCATCGCCGAGGGCGATTGGACAAGGACGAAGGAC 1358

Qy  247 GlyAlaSerSerLeuAlaProAspLeuArgAlaGlnIleAspGluThrLeuGluGlu---  265
          ::|:|:|
Db 1359 GGTGTCATCAAACGTCGAGGAGTCCAACACCTTCGGTGTGGACCTGGACTTCACCGAGGGC 1418

Qy  266 --------------IleThrProAlaTyrTyrValLeu-----GluLeuGlyGly      276
          :::|||||
Db 1419 ATGGCCCTTCGACAAGGGCTACCGTGTCCCCGTACACATGGTGACCGAGGCGTATGGAG   1478

Qy  277 LeuProLeuGlyAspAspTyrAlaAlaLysSerAlaLeuLeuValGlyLeuThrArgGluLys 296
          |||                                              :::
Db 1479 GCCGGAGACGTTCGAGGGCGAGGGCCCTGTCCGACGTCGACAACGATCCGGTTCGATGGAC  1538

Qy  297 IleLeu-------------------------PheLeuArgMetThrAlaAlaGluIleVal 317
          :::|||
Db 1539 CTGCTGCCCGCTGCTGGAGAAGGTCATCCAGGGCGGGGTGGGCTCCAAAGCCGCTGCTGATCATC 1598

Qy  318 PheMetAsnGluAla-------------------------------PheLeuArgMet   332
          |||
Db 1599 GCCGGAGGACGTTCGAGGGCGAGGGCCCTGTCCGACGTCGACAACGATCCGGTTCGAT    1658

Qy  333 AspLeuPheValAlaThrProSerArgAsnIleProAlaGluSerPheGluValTyrGluVal 352
          |||
Db 1659 TTCAACGACCGGTTCGGCGTCAAGGCCGCCCGGCCTTCGGACGGCGGATGCGCTCGAG    1718

Qy  353 AlaLeuAlaLeu----------------------------ValAlaGlnAlaPheIle   362
          |||
Db 1719 GACATGGCCCACCCTTCACCCGGTGCCACCGTCATCGCCGAG--------GAGGTC     1763

Qy  363 GlyLysGlyProHisLeuLeuGlnHisAspAlaAspLysGlnIleAsnAla           382
          |||
Db 1824 ACCAAGGACGACGACGACCATCGTGGACCTTCGGAGGAAGGACGGTTCCAGGGC        1880

Qy  383 LysValMetAlaMetGluIleProAlaMetLeuTyrArgAspThrArgAsnAsnTrpGluIle 402
          :::
Db 1881 ------CCGGTTCGCCCAGATCAAGGCCGGACTCGGAGTCGGACTCGGACACCGGC      1934

Qy  403 AspPheGlyLeuGluArg------------------GlyLeuCysAlaLeuLeuIleGly  416
          |||
Db 1935 GAGAAGCTTCCAGGAGGCGCCTTCGCCAAGCTGCTGATCGTGCTGATGATCGGGC      1994

Qy  417 LysValAspGlyCysArgMetTrpLeuGlyLeuAspSerGlnTyrArg-----        435
          :::
Db 1995 GCGGCCACCGAG--------GTCCGAGCTGAAAGGAGGCAAGCACCACCGTCTG       2036

Qy  436 --------------AsnProIleValGluPheValLeuGluAsnSerAsn           448
          |||
Db 2037 GAGGACGGCCATCTCCGGCGACACCCCCGGGTCAGCGGAGGGCCATCGTTCTCCGGCGTCGGC 2096

Qy  449 Arg--------AspAspAsn                                          454
          |||                                           :::
Db 2097 TCCGCGCTGGTTCCACGCGCGTCCAAGGTTCCTTGGAGCGACAACCTCGGCGCCGGGGAG   2156

Qy  455 LeuProGlyLeuCysLysLeuLeuGluThr---------TrpLeuAla--           467
          |||:||
Db 2157 GCCACCGGTGTCGGCGGGTCGTTCGGCGCGTGGACCGCGTGGACGTCGATCGCGGAG     2216

Qy  468 --------------GlyValValPheProArgPheArgAspThrLysAspLysLysPhe  482
          |||
Db 2217 AACGCCCGGCCCTCGAGGGGCTGTACGGTCATC---ACCACCAAGGTGGCGGGAGCTC    2264
```

US-10-600-070B-2 (1-801) x US-09-057-969-1 (1-2969)

DB: US-09-057-969-1

```
RESULT 4
US-09-057-969-1
Sequence 1, Application US/09057969
Patent No. 6013451

GENERAL INFORMATION:
APPLICANT: WONG, VICTOR THI WONG
APPLICANT: PHANG, SENG MENG
APPLICANT: TAN, TIEN CHYE
TITLE OF INVENTION: BACILLUS STEAROTHERMAPHILUS DNA
TITLE OF INVENTION: POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
TITLE OF INVENTION: 3'-TO-5' EXONUCLEASE ACTIVITY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,969
FILING DATE: 09-APR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 674507-2001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2969 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
```

Alignment Scores:
Pred. No.:
Score: 9.55e-05
Percent Similarity: 140.00
Best Local Similarity: 37.4%
Query Match: 21.6%
                    3.4%
                    3%

Length: 2969
Matches: 193
Conservative: 141
Mismatches: 369
Indels: 192
Gaps: 46

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Qy    310 ------------------------ValGlyGlyLeuThrArgGlyLysPheMet-----------------  319
                                  |||  :::::|| ::::||
Db   1311 CGCTTGGCCTTGGCATGAGACGAGAAGAAAAACGATAGTTTGATTCAAAAGCGGCGCCGT          1370

Qy    320 ------------AsnGluAlaPheLeuArgMetThrAlaAlaGlyGluGlnVal---AspLeuPheVal       336
                        :::
Db   1371 CGGCGCTAAATGGGAAAAGGAAATCGGCTGGCGTCGGCGTCGTTGTTCGATCTGTTGCT               1430

Qy    336 1AlaThrProSerAsnIleProAlaGluSer----------------PheGluVa                     349
                        :::
Db   1431 GGCGCGCTTACTTGCTCGATCCGCGCAGGGCGGTTGCCCGGGTTGGCGAAAT                       1490

Qy    349 1TyrGluValAlaLeuAlaLeuValAlaGlnAlaAlaPheIleGly-----LysProHisGlu            368
                  |||
Db   1491 GCATCAGTACGAGGCCGTTGCGGATCGGAGTGAGCGGGTTCTATGGAAAAGGAGCGGGAC             1550

Qy    368 uLeuGlnAspAlaAspLysGlyGlnPheGlnGlnLeu------GlnGlnAlaLysValMetAl            386
                  :::
Db   1551 GGTTCCTTGATGAACCGACGCGTTGCCGAGCAGTCTTCGTGCAAGGCGGCCATTCGGC               1610

Qy    386 aMetGluIleProAlaMetLeuTyrAspThrArgAsnAsnThrGlu---IleAspPheGl              405
                  :::
Db   1611 GCTTGAAGAGCCGTTGATGGAACGCGCCACACAAGATCGGCTGCCGACCGA                       1670

Qy    405 yLeuGluArgGlyLeuCysAlaLeuLeuIleGly-------------LysValAs                    419
                  |||
Db   1671 GCTTCGAACACGGCCCTGGCTCAGTTTGGCCAATATGGGAATTTACTGGAGTGAAAGTGA             1730

Qy    419 pGluCysArgMet------TrpLeuGlyLeuAsp---SerGluAspSerGlnTyrArgAsnPr           437
                  :::
Db   1731 CACGAAGGCGCTTGACAGATGGGGGGGGGGGGAGCTCACCGCAGCAGCTGCAG                     1779

Qy    437 oAlaIleValGluPheValLeuGlnAsnSerAsnArgAspAspAsnAspLeuProGl                  457
                  :::
Db   1780 -GCCGGTCGGAGCGGCGCATTCAGCAACTCGGCCCAAGAGTTCAACATTAACTCGCCG--             1836

Qy    457 yLeuCysLysLeuGluThrTrpLeuPheProArgPheArgAspTh                             477
                  |||
Db   1837 ------------------AAACAGCTCCGGACG-                                        1877
```

RESULT 5
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.:
Score: 32.9
Score: 139.00
Percent Similarity: 32.1%
Best Local Similarity: 21.5%
Query Match: 3.4%
DB:

	Length:	4411529
	Matches:	206
	Conservative:	101
	Mismatches:	328
	Indels:	323
	Gaps:	47

US-10-600-070B-2 (1-801) x US-09-103-840A-1 (1-4411529)

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Qy     17 CysArgLeuProAlaThrThrLysLeuArgSerHisAsnThrSerThrIle       36
             |||:||||||||||
Db   3401725 TGCCGATTGCCCGCCGGCTGAGCCATCCGTCGTCGG---------------   3401678

Qy    613 sGlu------------AlaSerValLysIleLeuAlaLeuGlyValAlaIleGlyLeuIleSe    630
                               :::
Db   2265 GTTCCGGCGGCTGGTTGGACATCCATACGAAAACAGCCATGGACATTTCCATGTGACGA     2324
```

```
Db  3401677  TGCCTCTCGGAACTGCCGTTGCCGGGGCTAGGCCGGG ----------TTGACTTCTCGGVACTGCGGTVGCCGTNGCCGGTGCCGGGCGTCG
              ||||||                                      |||                              |||:::
Qy        57  SerSer------                                SerSerPheAlaThrAlaThrThrThrAlaThrLeuVal  71

Db  3401623  GGCCTCAGTTCCTCGCGCTGCGCCGACGCGGTGCCCGGACGGGTGCCCGGGATCTTG                              3401564
              |||||                                                                          :::
Qy        72  SerLeuProProSerIleAspArg                    ProGluArgHisValProIle---  86

Db  3401563  TCGTCTCCCGCGCCGGCTVATGCAGTG--TTGGGCCGGGTGCGCGAGGCCGGCGTCGAC                          3401505
              |||:::                                                                         :::
Qy       101  ------------LeuThrAspGlyIleArg--ArgAlaPheGluAlaArg--ValSer  114

Db  3401504  TACCACCGGCGGGGATCGACATGCTCGGAGGCGGACGCAAGCGACGCAAGCGAGACA                            3401448
              ||||||                                                                         :::
Qy       87   ---------ProIleAspPheTyrGlnValLeuGlyAlaGlnThrHisPhe---  100

Db  3401447  ACATACGGACACTGTTCGGAGGGCGGAGGGTCGGTGCTGATTCGCGGGCTTTGATG                             3401388
              ||||                                                                           :::
Qy       115  LysProProGlnPheGlySerPheSerAspAlaAla----------LeuIleSerArg  129

Db  3401387  ACAGATCCAGAGCTGCTGCGTGCTGCCGACGCAACCCGGCGCCTGACTTAGGTGGCCGA                          3401328
              ||||||                                                                         :::
Qy       130  ArgGlnIleLeuGluGlnAlaAlaCysGluThrLeuSerAsnProArgSerArgGluTyr  149

Db  3401327  GAGGAATTGGTTCGCCCCCGGCTGGCGACTGGCACCGACCCT                                          3401286
              |||:::                                                                         :::
Qy       150  AsnGluGlyLeuLeuAspAspGluIleAlaThrValIleThrArgAspValProTrpAspAla  169
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[Pairwise nucleotide/protein sequence alignment — Qy (query) and Db (database) rows continue across the full page in the same format.]

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;   APPLICATION NUMBER: 08/222,612
;   FILING DATE: 16-SEP-1994
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Fisher, Carlos A
;       REGISTRATION NUMBER: 36,510
;       REFERENCE/DOCKET NUMBER: GP94003.CP2
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 619-535-2807
;       TELEFAX: 619-546-7929
;       TELEX:
; INFORMATION FOR SEQ ID NO: 33:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 2631 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE:
;   ORIGINAL SOURCE:
;   FEATURE:
;       NAME/KEY: Coding Sequence
;       LOCATION: 1..2631
;       OTHER INFORMATION:
; US-08-436-664-33

Alignment Scores:
Pred. No.:
Score:                       0.000192
Score:                     136.50          Length:            2631
Percent Similarity:         37.2%          Matches:            191
Best Local Similarity:      21.3%          Conservative:       143
Query Match:                 3.4%          Mismatches:         364
DB:                              2          Indels:             200
                                           Gaps:                44

US-10-600-070B-2 (1-801) x US-08-436-664-33 (1-2631)

Qy    12 SerProPheGlnLeuCysArgLeuProProAlaThrThrLysLeuArgSerHisAsn 31
         :::||||||||:::
Db    47 GGCCCTTTTTCCGTTGCCGCTTTTGCATAACGATAAAGGGATTCATACGAACGACGTCT 106

Qy    32 ThrSerThrThrIleCysSerArgAlaSerLysTrpAlaAspArgLeuLeuSerAspPheAsn 51
         |||
Db   107 ACGGGTTTACGATGATGTTAAACAAAATTTGGGAGAAGACAGCCGACCCACATTCTCG 166

Qy    52 PheThrSerArgSerSerSerSerPheAlaThrAlaThr------ThrThrAla 68
         :::||||
Db   167 TGGCGTTT-GACCGCCGGGAAAACGACGTTCCGCCATGAAACGTTCCAAGACGCGAAAGGC 225

Qy    69 ThrLeuValSerLeuProProSerIleAspArgProGluArgHisValProIleProIle 88
         |||||
Db   226 GGCCGGCAGCAGACGACGCGGCCCGAACGTTCGGAACAGTTTCCGCTGCTCGCGGAATTGCTC 285

Qy    89 AspPheTyrGlnValLeuGlyAlaGln------ThrHisPheLeuThrHisAspGlyIleLeuArg 107
         |||:::::
Db   286 AAGGCGTACCGCCATCCCCCGCCCTTATGAGCTCGACCATTACGGACAGCGGCGATATTATCGGA 345

Qy   108 AlaPheGluAlaArgValSerLysProGlnPheGlyPheSerArgAspAspAlaLeuIle 127
         |||||
Db   346 ACGATGGCGCGGCCGCGGGCTGAGCCGAGA------GGGTTTGCAGTGAAAGTCATTTCC 396

Qy   128 SerArgArgGlnIleLeuGlnAlaAlaCysGluThrLeuSerAsnProArgSerArgArg 147
         |||:::||||
Db   397 GGCGACCGGCGATTTAACCAG---------CTTGCGTTCCCCGCCAAGTGACGGTG 441

Qy   148 GluTyr---AsnGluGlyLeuLeuAspAspAspGluGlnAlaThrValIleThrAspVal--- 165
         :::||:::||||
Db   442 GAGATTACGAAAAAAGGGATTACCGACATCGAGTCGTTCGTACACGCCGGAGACGTGTCGTGGAA 501

Qy   166 -------------------------------------------------------ProTrp 167
Db   502 AAATACGGCCTCACCCCGGAGCAAATTGTCGACTTGAAAAGGATTGATGGGGCCGACAAATCC 561
```

```
RESULT 6
US-08-436-664-33
; Sequence 33, Application US/08436664
; Patent No. 5874282
; GENERAL INFORMATION:
;   APPLICANT: RIGGS, MICHAEL G.
;   APPLICANT: SIVARAM, MATHOOR
;   APPLICANT: TUDOR, STARLA D.
;   TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS
;   TITLE OF INVENTION: STEAROTHERMOPHILUS
;   NUMBER OF SEQUENCES: 34
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Gen-Probe Incorporated
;       STREET: 9880 Campus Point Drive
;       CITY: San Diego
;       STATE: CA
;       COUNTRY: USA
;       ZIP: 92121
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/436,664
;       FILING DATE: 08-MAY-1995
;       CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/394,232
;       FILING DATE:
;       APPLICATION NUMBER: 08/307,410
;       FILING DATE: 16-SEP-1994
```

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Qy      577 alaArgProSerGluAsnPheGluThrAsnAsp--------------- 587
            :::  :::
Db  3399627 TGGCCCCCGACGAGCGTTTACGACGCCGCGGCCGGGGAGGCGTTTCTTGACGGCC 3399568

Qy      588 --------------TyrAlaIleArgAlaGlyValSerGluSerValAspGluThrT 603
                          :::||:::||
Db  3399567 CGCCGCGCACGCGCTGGCCGGCGGCCGCCGCCAAACGCGGGGATCACGGAC-----G 3399526

Qy      603 hrValGluMetSerValAlaAspMetLeuLysGlu------------------- 614
            |||::|
Db  3399525 TCTACGAGCTCGGCGCCGCCCGAGCGGATCGCCGCGGGCGGGGGCTATGTGTCGGAGGTGT 3399466

Qy      615 --AlaSer-ValLysIleLeuUalAlaGlyValValAlaIleGlyValLeuIleLeuSerLeuPheSer 633
              |:::  ||:::||
Db  3399465 TCGGCCGCTGGGTCAAGTGGTGGTGGCGGCAGCAAAGGGTGACCGGGGCGGCCGCCGTTAGGCTC----- 3399412

Qy      634 GlnLysTyrPheLeuLeuSerSerSerSerPheGlnArgLysAspMetValSerSerMet 653
            :::   :::
Db  3399411 ---GCCTATATGACGAGGAGGAGTTCAAACATC----CCCGCCGACCGCACTCCCAATCCA 3399361

Qy      654 GluSerAspValAlaThrThrIleGlySerValArgAlaAspAspSerGluAlaLeuProArg 673
            :::   |||
Db  3399360 CATGCCACGGCCCGAGCAAGGTGGCGCCCGAGCTCGGCACGACGCAAGCTCGCCCAGGTGCTC 3399301

Qy      674 MetAspAlaAlaArgThrAlaGluGluAsnIleValSerLeuSerLysTrp--------- GlnLys 688
            |||||
Db  3399300 TACCACGACTGGGGAACCGAGAACTACGACCAGAAGTGGTCGATCTCTTATGACCAGCGT 3399241

Qy      689 IleLysSerLeuAlaPheGly--------------- ProAspHisArgIleGluMet 702
            :::||
Db  3399240 TGCGTCGACTACGCCCCGGCGTTCGACCGCGATCGTGCCTGATGAGGTCATCGGCCAG 3399181

Qy      703 LeuProGluValLeuAspGlyArgMetLeuLysIleTrpThrAspArgAlaAlaAlaGluThr 722
            ||||||
Db  3399180 CTGCCC------------------------------TACGACCCGCGCACTGGAA-- 3399157

Qy      723 AlaGlnLeuGlyLeuValTyrAspTyrThrLeuLeuLeuLysLeu 736
            ||||||
Db  3399156 ------------CTGGGCTGTGTGGAACCGGATTCTTCTGCTCAACTTG 3399121
```

Qy   168 AspLysValProGly-----------AlaLeuCysValLeuGlnGlu 179
             :::||||| |||:|||||||||||||||
Db   562 GACAACATCCCTGGCGTGCCCCGGCATCCGGGAGAAAAAACAGCCCAAGCTGCTCAAGCAA 621

Qy   180 GlyGlyGluThrGlnLysValLeuArgGlyValGlnValAlaLeuLeuLysGluArgLeuPro 199
             |||:|| ::: |||||:|:||||:|||
Db   622 TCGGCACGGTCGAAAACTTACTGCATCCATCGATGAGATCAAAGGGAGAAGCTGAAA 681

Qy   200 LysSerPheLysGln-----------AspValValLeuValMetAlaAlaPheLeuAspVal 217
             |||:||| ::: |||||||||||:|
Db   682 GAAAATTTGCGCAATACCGGGAGTTTGGCGCTT-----TTAAGCAAACAGCTGGGCGCTATT 738

Qy   218 SerArgAspAla------------MetAlaLeuAspProProAspPheIleThrGlyTyrGlu 234
             ||| ||| :::
Db   739 TGCCGCGAGGCCCCGGTTGAGCTGACGGTCGAT-----GACAATGTTCTACAAGGAGAA 792

Qy   235 PheValGluValAlaLeuLysLeuLeuGlnGluGlyGlyValAlaSerSerLeuAlaProAsp 254
             :::|||||||||||||||||||||||||||||||||||||||||||||
Db   793 GACCGGGGAAAAGTGGTCGCCTTGTTCAGGAGCTGCGTTTCTCGACAAG 852

Qy   255 LeuArgAlaGlnIleAspGlu-----------ThrLeu 263
             ||| :::
Db   853 ATGGCCGCGTTCCAAACGGGATGAAAAGCCGTTCGCCCGGGATGATTTTGCGATCGCC 912

Qy   264 GluGluIleThrProArgTyrValLeuGluIleLeuGluLeu-----ProLeuGly 280
             :::   ::: |||||
Db   913 GACAGCGTCACGGACGAAAATGCTCGCCAGACAAAGCCGCTCGTCGGTGGAGGTGGGGC 972

Qy   281 AspAspTyr-AlaAlaLysArgLeuAsnGlyLeuSerGlyValArgArgAsnIleLeuTrpSe 300
             ||||| :::
Db   973 GACAACTATCACCATGCCCCCAATTGTCGGGATCGGCCT-----TGGCC 1014

Qy   300 rValGlyGlyGlyValAlaSer-AlaLeuValGlyGlyLeuThrArgGlyLysPheMetA 320
             ||| :::
Db 1075 GCGCTAAAATGGAAAGGAAATCGAACTCGCGCGGTCGTCTGTTGCTGGCCGGCT 1194

Qy   320 snGluGluAlaPhe----------ProLeuGly 323
             :::
Db 1015 AACGAACGCGGCGGGTTTTCCTGCGCCGGCGCTCGGCGTCGGCATCCGAAATTTCTC 1074

Qy   324 ------------LeuArgMetThrAlaLeuAlaMetLeuuTyrAsp 338
             |||
Db 2134 ATCGTGTACGGACCAATTAGTGAT----TACGGTCTCGGCGCAAAACTTGAACAATTACGGCGAAA 2190

Qy 1075 GCTTCGGCCTTGGCGATGAGCACGCGGCTCGCGCCGCCGGGCCGTC 1134

RESULT 7
US-09-135-642-33

Sequence 33, Application US/09135642
; Patent No. 6066483
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATHOOR
; APPLICANT: TUDOR, STARLA D.
; TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS
; TITLE OF INVENTION: STEAROTHERMOPHILUS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/394,232
; FILING DATE:
; APPLICATION NUMBER: 08/307,410
; FILING DATE: 16-SEP-1994
; APPLICATION NUMBER: 08/222,612
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94003.CP2
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2631
; OTHER INFORMATION:

US-09-135-642-33

Alignment Scores:
Pred. No.:
Score: 0.000192
Score: 136.50
Percent Similarity: 37.2%
Best Local Similarity: 21.3%
Query Match: 3.4%
DB:

US-10-600-070B-2 (1-801) x US-09-135-642-33 (1-2631)

Length: 2631
Matches: 191
Conservative: 143
Mismatches: 364
Indels: 200
Gaps: 44

Qy   12 SerProPheGlnLeuCysArgLeuProProAlaThrThrLysArgSerHisAsn 31
             ::|::|||||| ||::
Db   1 GCGCCTTTTCGCGGTTGCCCCCTTTTGCATAACGATAAAGGGATTCATACGAACGCAGTCT 106

Qy   32 ThrSerThrThrIleCysSerAlaSerLysTrpAlaAspArgLeuLeuSerAspPheAsn 51
             ||| ||| ::::| |||:::
Db   32 GCGCTAAAATGGAAAAGGAAATCGAACTCGGCGGCGTCGTCGTTCGATCGTCGTTGGCGCT 324

Db   107 ACGGGGTTTACGGATGATGTTGTTAAACAAAAATTTTGGGGGAGCAGCAGCCGACCCACATTCTCG 166

Qy   52 PheThrSerAspSerSerSerSerSerPheAlaThrAlaThr------ThrThrAla 68
             |||::|||::   :::::|:   :::
Db   167 TGGGCGTTT-GACGCGGAAAACGACGTTCGGCCATGAAACGGTTCAAGAGACGGAAAGGC 225

Qy   69 ThrLeuValSerLeuProProSerIleAspArgProLeuArgHisValProIleProIle 88
             :::||| :::
Db   226 GGCCGGCCAGGAGACCCGGCCGGGACTGTCGAACAGTTCGGCTCCTCGCGGAATTGCTC 285

Qy   89 AspPheTyrGlnValLeuGlyAlaGln---------ThrHisPheLeuThrAspGlyIleArgArg 107
             |||::: |||::|||
Db   286 AAGGCGTACCGCCATCCCGCGCCTATGAGCTCGACCATTACGAGGGGACGAATATATCGGA 345

Qy   108 AlaPheGluAlaArgValSerLysProProGlnPheGlySerProAlaAlaLeuIle 127
             ||||||| :::
Db   346 ACGATGGGCGGGGCGCTGAGCGAGGAA------GGGTTTGCAGTGAACGTCATTCC 396

Qy   128 SerArgArgGlnIleLeuGlnAlaAlaCysGluThrLeuSerAsnProArgSerArgArg 147
             :::|||||| ---
Db   397 GGCGACCCGGCGGATTTAACCCAG-----------CTTGCTTCCCCGCAAGTGACGGTG 441

Qy   148 GluTyr---AsnGluGlyLeuLeuAspArgGluGluAlaThrValIleThrAspVal-- 165
             ||| :::|||::: |||:::
Db   442 GAGATTACGAGAAAAAAGGAATTACCGACATCGAGTTGTACACGCGGGACACGGTCGTGGAA 501

Qy   166 --ProTrp 167
Db   502 AAATACGGCCTCACCCCGGAGCAAAATTGTCGACTTGAAAGGATGACAAATCC 561

Qy   168 AspLysValProGly----------------------AlaLeuCysValLeuGlnGlu 179
             :::   :::
Db   562 GACAACATCCCTGGCGTCCCCGGCGCATCGGGGAAAAAACAGCCGTCAAGCTGCTCAAGCAA 621

Qy   180 GlyGlyGlyThrGlyIleIleValValGlyGluAlaLeuLeuLeuLysGlyArgLeuPro 199
             |||||| :::|||:::
Db   622 TTCGGCACGGTCGAAAACGTACTGGCATCGATGAGGATCAAAGGGGAGGAAGCTGAAA 681

Qy   200 LysSerPheLysGln------AspValValMetAlaLeuAlaPheLeuAspVal 217
             :::|||||| :::
Db   682 GAAAATTTGCGCCAATACCGGAGGATTTGGGCGTTT-TTAAGCAAACAGCTGGCGGCTATT 738

Qy   218 SerArgAspAla--------MetAlaLeuAspProProAsnPheIleThrGlyTyrGlu 234
             ||||||::|||| |||
Db   739 TGCCGCGACGCCCCGGGTTGAGCTGACGCTCGAT-----GACAATTGTCTACAAAGGAGAA 792

Qy   235 PheValGluGluAlaLeuLeuLeuGlnGlyIleGlyAlaSerSerLeuAlaProAsp 254
             ::: |||
Db   793 GACCGGCGAAAAAGTGGTCGCCTTGTTCAGGAGCTCGGATTCCAGTCGTTTCTCGACAAG 852

Qy   255 LeuArgAlaGlnIleLeuAspGlu----------------Thr 263
             ::: |||
Db   853 ATGGCCGGTCCAAACGGATGAAGGCGAAAAAGCCCGCTCGCCGGGATGGATCGCC 912

Qy   264 GluGlnIleThrProArgTyrValLeuGluGluGlyLeu------ProLeuGly 280
             :::   :::
Db   913 GACAGCGTCACGGACGAAATGTCTGCCGACAAAGCCGCTCGTCGTTGGCGTTGGCG 972

Qy   281 AspAspTyr-AlaAlaLysArgLeuAsnGlyLeuSerGlyValArgAsnIleLeuTrpSe 300
             |||::||| |||||| :::
Db   973 GACAACTATCACCATGCCCGATTGTCGGGGATCGGCT------TGGCC 1014

Qy   300 rValGlyValGlyValGlyAlaSer-AlaLeuValAlaGlyTyrLeuThrArgGlyLysPheMetA 320
             ||||||| ::: |||:::
Db   1015 AACGAACGCGGCGCGGGTTTTCCTGCGCCCGGAGACGGCGCTCGCCGGATCCGAAATTCTC 1074

Qy   320 snGluAlaPhe---------- 323
             |||:::
Db   1075 GCTTGGCTTGGCCGATGAGACAGAGAAAAAAACGATGTTGATTCAAAGCCGGCGGCCGTC 1134

Qy   324 ------------------LeuArgMetThrAlaAlaGlnGlnVal-AspLeuPheValAlaThr 338
                              |||||| :::|||:::
Db   1135 GCGCTAAAATGGAAAAGGAAATCGAACTCGGCGGCGTCGTCGTTCGATCGTCGTTGGCGCT 1194

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Qy  339 ProSerAsnIleProAlaGluSer------------------------PheGluValTyrGlu 351
                                                    CGCTTCGAGGTCTACGAG
                                                    ::::::::::
Db 1195 TACTTGCTCGAATCCCGGCAAGGGCCGGGCGGGCCGAGCGGTTGCCCGGGTGGCGAAATGCATCAG 1254

Qy  352 ValAlaLeuAlaLeuValAlaGlnAlaPheIleGlyLys 364
                                        ||||
Db 1255 TACGAGGCGCGTGCGATCGGATGAGAGCGGTCGGAAGGAAGCGGACGGTTCCT 1314

Qy  365 ---LysProHisLeuLeuGlnAspAlaAspLysGlnPheGlnLeuGlnIleAlaLys 383
              ::
Db 1315 GATGAACCGACGGTTCGCGAGCCATCTCGCCCGC 1359

Qy  384 ValMetAlaMetGlyIleLeuProAlaMetLeuTyrArgAspThrArgAsnAsnTrpGlu---Ile 402
        |||                                                     :::  :::
Db 1360 ATTTTGGCGGCTTGAAGAGCCCTTGATGGACGAACTGCGCCGACAAGATCCGGCTG 1419

Qy  403 AspPheGlyLeuGlyLeuArgGlyLeuCysAlaLeuLeuIleGly--------------- 416
        ||||                                        ------
Db 1420 CTGACCGAGCTCGAACAGCCCCTGGCTGGCGCATTTTGGCCAATATGGGAATTTACTGGAGTG 1479

Qy  417 LysValAlaAspGluCysArgMet------TrpLeuGlyLeuAsp---SerGluAspSerGlnTyr 434
        |||                   :::               :::
Db 1480 AAAGTGGACAACGGAACGGCGGCTTGAACAGATGGGGGGCGGAGCTCACCCGAGCCAGCTGCAG--- 1536

Qy  435 ArgAsnProLaIleValGluPheValLeuGluAsnSerAsnArgAsnAspAsnAspAsp 454
        ------      :::  :::
Db 1537 ------------GCGGTCGAGCGCGCGCATTTACGAACTCGCCCGAGAGTTCAACATTAAC 1587

Qy  455 LeuProGlyLeuCysLysLeuLeuGluThrTrpLeuAlaGlyValValPheProArgPhe 474
        |||                   :::|:::|||
Db 1588 TCGCCG------AAACAGCTCGGGACG 1626

Qy  475 ArgAspThrLysAspLysPheGlyLeuGlyLeuArgGlyLeuCysAlaLeuLeuIleGly 494
        :::  |||                                :::
Db 1627 CAGCTCCCGGTGTTGAAAAAGACAAAACCGGC---TATTCGACTTCAGCCCATGTGCTT 1683

Qy  495 SerTyrTyrLeu---GluArgValGlnValValGlnGlySerProLeuLeuAlaAlaAlaThr 513
        :::|:::|||                               :::
Db 1684 GAGAAGCTTGCACCGCACCATGAAAATCGTCGAA------CATATTTGCATTACCGCCCAA 1737

Qy  514 MetAlaArgIleLeuGlyAlaGluHisValLysAlaSerAlaMetGlnAlaLeuGlnLysVal 533
        |||                                :::
Db 1738 CTCGGCGAAGCTGCAGTCAACGTATATTGAA---GGGCTGCTGAAAGTAGTGTGCACCCCGTG 1794

Qy  534 PheProSerArgThrArgAspArgAsnSerAlaGluProLysAspSerValGlnGluThr--- 552
                                                :::
Db 1795 ACGGGCAAAGTGCACACGATGTTCAAATCAGGGG---------TTGACGCAAACCGGG 1842

Qy  553 ---ValPheSerValAspProValGlyAsnAspGlyArgAspGlyGluProGlyVal 571
              |||:::|||                        :::
Db 1843 CGCCTCAGCTCCGTCGAACCGAATTTGCAAAAACATTCCGGATTCGGCTTGAGGAAGGCGCG 1902

Qy  572 PheIleAlaGluAlaValAlaArgProSerGlu------------AsnPhe 583
        |||                             :::||
Db 1903 AAAATCCGCGCAGGCGGTTCGTTGCGTGCCGGACTGGGCTCTCATCTTTGCGGCCGACTAT 1962

Qy  584 GluThrAsnAspTyrAlaIleArgAlaGlyValSerGluSerValAspGluThrThr 603
        |||                                :::
Db 1963 TCGCAAAATCGAGCTGCGCGGTCTCGCGCCCATATCGGGGGAA------GATGACAATTG 2013

Qy  604 ValGlu------------------MetSerValAlaAsp 610
        |||               :::|||
Db 2014 ATTGAACGGTTCCGGCGGGGTTGGACATCCATACGACCATGGACATTTTCCAT 2073

Qy  611 MetLeuLysGlu------------AlaSerValLysIleLeuValAlaGlyValAlaIleGly 627
        |||               :::|||
Db 2074 GTGAGCGAAGAGAGACGTGACACGCCAAACATGCGCCGCCAAGACGGGAAGGCCGTCAATTTTGGC 2133

Qy  628 LeuIleSerLeuPheSerGlnLleLysTyrPheLeuGlySerSerSerSerProGluGlnArgLys 647
        |||       :::|||
Db 2134 ATCGTGTACGGCAGCATTAGTGAT---TACGGTCTGGGCGAAAACTTGAACAATTACGGCAAA 2190
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Qy  648 AspMetValSerSerMetGluSerAspValAlaAlaThrIleGlySerValArgAlaAspAsp 667
        :::                                                      |||:::
Db 2191 GAAGCGGCTGAATTTATTGAGCGGATATTTGGCCAGTTTTCCAGGGTGAAAG------ 2241

Qy  668 SerGluAlaLeuProArgMetArgAspAlaArgThrAlaGluAsnIleValSerLysTrpGln 687
        :::                                                       :::
Db 2242 -----CAAATATGGACAACATTTGTGCAAGAA---GCG 2271

Qy  688 LysIleLysSerLeuAlaPheGlyProAspHisArgIleGluMetLeuProGluValLeu 707
        |||
Db 2272 AAACAAAAAGCGTATCGTGACGACGCTGCGTCCGCGGCCGCTATTTGCCCGGATATTACA 2331

Qy  708 AspGlyArgMet---LeuLysIleThrTrpThrAspArgAlaAlaAla---GluThrAlaGlnLeu 725
        :::         :::                                 |||
Db 2332 AGCCGGCAAACTTCAACGTCCGCAGCTTCCCGAGCAGGCGCGGATGAACACACCGGATCCAA 2391

Qy  726 GlyLeuValTyrAspTyrThrLeuLeuLysLeuSerValAsp---SerValThrValSer 744
        :::                                       |||:::|||
Db 2392 GGGAGTGCCGGCTGAT---ATTATTAAAAAGGATGATGATCTTAAGCGGTGAGGCTGGCC 2448

Qy  745 AlaAspGlyThrArgAla------------------------LeuValGluAla 754
        :::                                       |||
Db 2449 GAAGAACGGGCTGCAGCGGCCGGCCTGTTGCTGCAAGTGCATGACGAACTCATTTTGGAGCGG 2508

Qy  755 ThrLeuGluGluSerAlaCysLeuSerAspLeuValHisProGlu 769
        ||||||||
Db 2509 CCGAAAGGAGGAAATCGACGACGGCGTTGCGCCGCCTCGTT---CCAGAG 2550
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RESULT 8
US-08-394-232A-33
Sequence 33, Application US/08394232A
Patent No. 6100078
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATHOOR
; APPLICANT: TUDOR, STARLA D.
; TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILU
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,232A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/307,410
; FILING DATE: 16-SEP-1994
; APPLICATION NUMBER: 08/222,612
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94003.CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE:       cDNA
; HYPOTHETICAL:        NO
; ANTI-SENSE:          NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
;   NAME/KEY:          Coding Sequence
;   LOCATION:          1...2631
;   OTHER INFORMATION:
US-08-394-232A-33

Alignment Scores:
Pred. No.:
Score:                 136.50
Percent Similarity:    37.2%
Best Local Similarity: 21.3%
Query Match:           3.4%
DB:

US-10-600-070B-2 (1-801) x US-08-394-232A-33 (1-2631)

Length:       2631
Matches:      191
Conservative: 143
Mismatches:   364
Indels:       200
Gaps:         44
```

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Qy      12 SerProPheGlnLeuCysArgLeuProProAlaThrThrLysLeuArgSerHisAsn 31
           ::|||||||||                                      :: ||
Db      47 GCGCCTTTTCGCCTTGCGCCGCTTTTGCAATAACGATAAAAGGGATTCATACGACAGTCT 106

Qy      32 ThrSerThrThrIleCysSerAlaSerLysTrpAlaSerAspPheAsn 51
           |||:::                                    |||:::
Db     107 ACGGGTTTACGATGATGTTAAACAAAAATTTTGCGGAAGACAGCCGACCCACATTCTCG 166

Qy      52 PheThrSerAspSerSerSerSerPheAlaThrAlaThr----- 68
           |||:|||                             ThrThrAla
Db     167 TGGCGTTT-GACGGCCGGGAAAACGACGTTCCCGCATGAAACGTTCATACGACAGAGGC 225

Qy      69 ThrLeuValSerLeuProProSerIleAspAsnArgProGlnHisValProIleProIle 88
           |||:::                                        :::
Db     226 GGCCGGCAGCAAGACGACGCCGCCCGAACTGTCGGAACAGTTCCGCTGCTGCGCGAATTGCTC 285

Qy      89 AspPheTyrGlnValLeuGlyAlaGln---ThrHisPheLeuThrAspGlyIleLeuArgArg 107
           :::                       |||:::
Db     286 AAGGGCTACCCGCCATCCCGCCTATGACGATTACGACCATTACGACGAGTAATATCGGA 345

Qy     108 AlaPheGluAlaAlaArgValSerLysProProGlyInPheSerGluAspAspAlaLeuIle 127
           :::                                                :::
Db     346 ACGATGGCGCGGCGGCGGTCGGTAGCGGGAGAA--GGGTTGCAGTGAAAAGTCATTCC 396

Qy     128 SerArgArgGlnIleIleLeuGlnIleAlaAlaAlaCysGluThrLeuSerAsnProArgSerArgArg 147
           |||:::                                    CTTGCTTCCCCGAAGTGACCGTG
Db     397 GGCGACCGGGATTACCCAG------- 441

Qy     148 GluTyr---AsnGluGlyLeuLeuAspAspGluValAlaThrValIleThrAspVal--- 165
           |||                                                   :::
Db     442 GAGATTACGAAAAAAAGGATTACCGACATCGAGTCGTACACGCCGGAGACGGTCGTGGAA 501

Qy     166 ------ProTrp 167
           :::
Db     502 AAATACGGCCTCACCCGGACGCAAAATTGTCCGACTTGAAAGGATTGATGGGGACAAATCC 561

Qy     168 AspLysValProGly-------AlaLeuCysValLeuGlnGlu 179
           |||                                 :::
Db     562 GACAACATCCCTGGCCGTGCCCGGCAAAAACAGCGCGTCAAGCTGCTCAAGCAA 621

Qy     180 GlyGlyGluThrGluIleLeuValLeuValGlyIleAlaArgLeuPro 199
           |||:::                                    SerLeuPro
Db     622 TTCGGCACGCTGCGAAAACGTACTGGCATCGATGAGATCAAAGGGAGAGAAGCTGAAA 681

Qy     200 LysSerPheLysGln-----AspValValLeuValMetAlaLeuAlaPheLeuAspVal 217
           |||:::                                             :::
Db     682 GAAAATTTGGCGCAATACCGGGACTGGCCGCTT--TTAAGCAAAACAGCTGGCCGTATT 738

Qy     218 SerArgAspAla-----------MetAlaLeuAspProProAspPheIleThrGlyTyrGlu 234
           |||:::                                             :::
Db     739 TGCCCGCGACGCCCCGGTTGAGCTCGGATCGGATCGGAT---GACATTGTCTACAAAGGAGAA 792

Qy     235 PheValGluGluValAlaLeuGluLysLeuGluGlnGluGlyGlnGlyAlaSerSerLeuAlaProAlaAsp 254
           :::                                    GACCCGGGAAAAAGTGGTCGCCGCTTGTTTGTTCAGGAGCTCGTTTCTCGACAAG
Db     793 GACCCGGGAAAAAGTGGTCGCCGCTTGTTTGTTCAGGAGCTCGTTTCTCGACAAG 852

Qy     255 LeuArgGlnAlaGlnIleIleAspGlu--------ThrLeu 263
           :::
Db     853 ATGGCCGGTCCAAACGGTATGAAGGGCGAAAAACCGGCTTCGCCGGGATTCCCAGTCGGC 912

Qy     264 GluGluIleThrProArgTyrValLeuGluGlyLeuGlyLeu------ProLeuGly 280
           |||
Db     913 GACACGCGTCACGGACGAGAAATGCTCGCCGACAAAGCGCCGCTGGTGGAGGTGGGC 972

Qy     300 rValGlyGlyGlyGlyAlaSer-AlaLeuValGlyGlyLeuThrArgGlyGluLysPheMetA 320
           |||:::
Db    1015 AACGAACGCGGCGGGCGGTTTTCCTGCGGCCCCGGAGACGGGCTCGCCGGATCCGGAAATTTCTC 1074

Qy     281 AspAspTyr-AlaAlaLeuAspLeuAsnGlyLeuSerGlyValArgAsnIleLeuIlePhe 300
           |||:::
Db     973 GACAACTATCACCCATGCCCCGATTCTCCGGGGATCGGCT---TGGCC 1014

Qy     320 snGluAlaPhe----------- 323
           ||:::
Db    1075 GCTTGGCCTCGGCGATGAGAGGAAGAAGAAAAAACGATGTTTGATTCAAAAGCGGGGGCCGTC 1134

Qy     324 -----------LeuArgMetThrAlaAlaGluGlnVal--AspLeuPheValAlaThr 338
           :::
Db    1135 GCGGTAAAATGGAAAGGAAATCGAACTGCGCGGCGTCGTGTTCGATCGTGTTGCTCGGCT 1194

Qy     339 ProSerAsnIleProAlaGluSer----------PheGluValTyrGlu 351
           :::
Db    1195 TACTTGCTCGATCGGCGGCCGGAAGCCGACGTTGCCGGCGTTGGGGGAAAATGCATCAG 1254

Qy     352 ValAlaLeuAlaLeuValAlaGlnAlaPheIleGlyLysLys--- 364
           :::
Db    1255 TACGAGCGCGGTGCCGGATCGGATGAGGCGGTCTATGGAAAAGGAGGACGGTTCCT 1314

Qy     365 ---LysProHisLeuLeuGlnAspAlaAspLysGlnPheGlnGlnLeuGlnLeuAlaLys 383
           |||:::
Db    1315 GATGAACCGAACGCTTGCCCAGCCATCTCGCCCGC----AAGGCGCGGCGCC 1359

Qy     384 ValMetAlaMetGluIleProAlaAlaMetLeuTyrAspThrArgAsnAsnTrpGlu---Ile 402
           |||:::
Db    1360 ATTTTGGGGCGGCTTGAAGAGCCGTTGATGGACGAACTGCGCACACAAGATCGGCTG 1419

Qy     403 AspPheGluGlyTyrLeuCysGlyAlaLeuLeuIleIleGly----------- 416
           |||:::
Db    1420 CTGACCGGAGCTCGAACACGCGTCTGGCGTCGCATTTGGCCAATATGGAGTG 1479

Qy     417 LysValValAspGluCysArgMet------TrpLeuGlyLeuAsp--SerGluAspSerGlnTyr 434
           |||:::
Db    1480 AAAGTGGACACGAACAGGCGCTTGAACAGATGGCGGGAGACTCACGGAGGCGCAG---1536

Qy     435 ArgAsnProAlaIleValGluPheValLeuAsnSerAsnArgAspAspAspAsp 454
           |||:::
Db    1537 ------GCGGTCGAGGCGGCGCCATTACGAACTGCGGCCAAGAGTTCAACATTAAC 1587

Qy     455 LeuProGlyLeuCysLysSerLeuLeuGluThrTrpLeuValLeuValPheProArgPhe 474
           :::
Db    1588 TCGCCG------------GTTTTATTTGACAAGCTG 1626

Qy     475 ArgAspThrLysAspLysPheLysGlyAspTyrTyrAspAspProMetValLeu 494
           |||:::
Db    1627 CAGCTCCCGGTGTTGAAAAAGACAAAAAGCCGGC---TATTCGACTTCAGCCGATGTGCTT 1683

Qy     495 SerTyrLeu--GluArgValGlyValValGlnGlySerProLeuAlaAlaAlaAlaThr 513
           |||:::
Db    1684 GAGAAGCTTGCACCGCACCATGAAATCGTCGAA------CATATTTCGACATAAGGCCAA 1737

Qy     514 MetAlaArgIleGlyAlaGluHisValLysAlaSerAlaMetGlnAlaLeuGlnIleLysVal 533
           |||:::
Db    1738 CTCGGCAAGCTCCAGTCGATCGAACGTATAATTGAA---GGGCTGCTCGAAAGTGGTGCACCCCGTG 1794

Qy     534 PheProSerArgTyrThrAspArgAsnSerAlaGluProLysAspValGlnGluThr--- 552
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SEQUENCE CHARACTERISTICS:
  LENGTH: 2631 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
  NAME/KEY:
  LOCATION:
  NAME/KEY: CDS
  LOCATION: 1..2631
DB:
PCT-US95-04080-33

US-10-600-070B-2 (1-801) x PCT-US95-04080-33 (1-2631)

Alignment Scores:
Pred. No.:   0.000192
Score: 136.50
Percent Similarity: 37.2%
Best Local Similarity: 21.3%
Query Match: 3.4%

Length: 2631
Matches: 191
Conservative: 143
Mismatches: 364
Indels: 200
Gaps: 44
              6

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Qy  12  SerProPheGlyIleLeuCysArgLeuProProAlaThrThrLysLeuuArgArgSerHisAsn  31
        :::||||||
Db  47  GCGCCCTTTTCCGGGTTTGCCCGTTTGCCGTTTTTGCATAACCGATAAAGGGATTCATACGAAGCCAGTCT  106

Qy  32  ThrSerThrThrIleCysSerSerAlaSerLysTrpAlaAspAspArgLeuuLeuuSerAspPheAsn  51
        :::||:::||
Db 107  ACGGGTTTACGATGATGTTAAACAAAATTTTGGCGGAAGAGCCGGAACCACATTCCG  166

Qy  52  PheThrSerAspAspSerSerSerSerPheAlaThrAlaThr------ThrThrAla  68
        :::       ::::|||
Db 167  TGGCGTTT-GACCGCCGGGGAAAACGACGTTCCGCCATGGAAACGTTCCAAGACGCGAAAGC  225

Qy  69  ThrLeuValSerLeuProProSerIleAspProArgProGluArgHisValProIleProIle  88
        :::
Db 226  GGCCGGCGCAGCAGACGACGGCCGCCGGAACTGTCGGAACAGTTTCCGCTGCGGAATTGCTC  285

Qy  89  AspPheTyrGlnValLeuGlyLysTyrGlyAlaGln---ThrHisPheLeuuThrArgGlyIleLeuArgArg  107
        :::||:::
Db 286  AAGGGCGGTTACCGACCATCCCCGCCTATGAGCTCGACAGCTCGACGATATTATCGGA  345

Qy 108  AlaPheGluAlaArgValSerLysProProGlnPheGlyPheSerAspAspAlaLeuuIleLeuuIle  127
        :::||:::||
Db 346  ACGATGCGGCGGCGCGTGCCGAGCGAGAGA---  396

Qy 128  SerArgArgGlnIleLeuGlnAlaAlaCysGluThrLeuuSerAsnProArgSerArgArg  147
        :::       :::
Db 397  GGGCGACGGCGATTTAACCCAG---CTTGCTTCCCCGCAAGTGACGGTG  441

Qy 148  GluTyr---AsnGluGlyIleLeuuLeuuAspAspGluuGluuAlaThrValIleThrArgAspVal---  165
        ::::::    :::||
Db 442  GAGATTACGAAAAAAGGGGATTACCGACATCGAGTCGTACACGCCCGGAGACGTTCGTCGAA  501

Qy 166  ------ProTrp  167
Db 502  AAATACCGGCCTCACCCCCGAGCGAAAATTGTCGACTTGAAAGGATTGAATGGGCCGGACAAATCC  561

Qy 168  AspLysValProGly---AlaLeuuCysValLeuuGlnGlu  179
        :::|:::    :::||:::
Db 562  GACAACAATCCCTGGCCGTGCCCCGCGGAAAAAACAGCCGTCGAAGCTGCTCAAGCAA  621

Qy 180  GlyGlyGlyThrGlyIleIleValLeuuValGlyGlyAlaLeuuLeuuLysGlyuArgGluuLeuuPro  199
        |||
Db 622  TTCCGGCACCGTCGAAAACGTTACTGGCCATCGATCGAATCGAATGAGAGCTTGAAA  681

Qy 200  LysSerPheLysGlyGln---AspValValLeuuValMetAlaLeuuLeuuAlaPheLeuuAspVal  217
        :::||:::    ::::::
Db 682  GAAAATTTGCGCCAAATACCGGGATTTGGGCGCTT---TTAAGCAAAACAGCTGGCCGCCGCTATT  738

Qy 218  SerArgArgAspAla---MetAlaLeuuAspProProAspPheIleThrGlyTyrGlu  234
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Db 739  TGCCGCGACACGCCCCCGGGTTGAGCTGACGCTCGAT-----GACATTGTCTACAAAAGGAGGAA  792
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Qy 1795  ACGGGCAAAGTGCACACGATGTTCAATCAGGCG------------TTGACGCAAACCGGG
         :::|||                              ::::|||
Db 1843  CGCCTCAGCTCCGTCGGAACCGAATTGCAAAAACATTCCAATTCGGCTTGAGGAGGGCCG  1902

Qy  553  ---ValPheSerValAspProValGlyAsnAsnValGlyArgAspGlyValGluProGlyVal  571
         ::::|||
Db  572  PheIleAlaGluAlaValAlaValAlaArgProSerGlu------------AsnPhe  583

Qy 1903  AAAATCCCCAGGCGGTTCGTTCGTCCGGTCGGAGCCGGACTGGCCTCATCTTTGCGGCGACTAT  1962
         ::::|||
Db  604  ValGlu---------------------------------MetSerValAlaAsp  610

Qy 2014  ATTGAAGCGGTTCCGGCCGCGGTTGGACATCCATACGAAAAACAGCCATGGACATTTCCAT  2073

Qy  611  MetLeuuLysGlu---------AlaSerValLysIleLeuuAlaAlaGlyValAlaIleGly  627
         :::||:::::::||
Db 2074  GTGACGGAAGGAAGAGCCGTGACAGCCAACATGCGCCCCCAATATCGCAATTTTGGC  2133

Qy  628  LeuuIleSerLeuuPheSerGlnLysTyrPheLeuuLysSerSerSerSerPheGlnArgLys  647
         :::||
Db 2134  ATCGTGTTACGGCCATTAGTGAT---TACGGTCTTGGCCGCGAAAACTTGAACATTACGCGCAAA  2190

Qy  648  AspMetValSerMetGluSerAspValAlaIleThrGlyLysSerValAlaArgAlaAspAsp  667
         ::::::
Db 2191  GAAGCGGGCTGAATTTATTGAGCGATATTTTGCCAGTGTGTAAAG------  2241

Qy  668  SerGluuAlaLeuuProArgMetAspAlaArgThrAlaGluuAsnIleuSerIleLysTrpGln  687
         :::                   ::::::
Db 2242  -----------------------CAATATGGACAACATTGTCCAAGAA---GCG  2271

Qy  688  LysIleLysSerIleuAlaPheGlyProAspHisSerArgIleGluuLeuuMetLeuuProGluuValLeuu  707
         ::::::|||
Db 2272  AAACAAAAAGGGTATGTGACGAGCCTGCTGTCCATCGGGCCGTTATTTTGCCGGATTAATTACA  2331

Qy  708  AspGlyArgMet---------LeuuLysIleTrpIleThrArgArgAlaAla---GluuThrArgAlaGlnLeuu  725
         :::
Db 2332  AGCCGCAACTTCAAGCTCCGCAGCTTCGCCGGAGCGGACCGGCCGGATCGGATCCAA  2391

Qy  726  GlyLeuuValTyrArgAspTyrArgLeuuLeuuLeuuLysSerValAsp---SerValThrValSer  744
         :::       :::||
Db 2392  GGGAGGTGCCCTGAT---ATTATTAAAAAGCGATGAGTCGGCTGCGC  2448

Qy  745  AlaAspGlyThrArgAla---------LeuuValGluuAla  754
         :::|||
Db 2449  GAAGAACGGGCTGCGCGGCGCCCTGTTGCTGCAAGTGCATGACGAACTCATTTTGGAGGCG  2508

Qy  755  ThrLeuuGluuGluuSerArgAlaCysLeuuSerAspLeuuValHisProGlu  769
         :::||:::||
Db 2509  CCGAAAGAGGAAATCGAGGCGGCTGTGTCCGCGCCTTCGTT---CCAGAG  2550
```

```
Qy         235 PheValGluGluAlaLeuLysLeuLeuGlnGluGluGlyAlaSerSerLeuAlaProAsp 254
                     |||:::   :::   |||   ||||||   |||      |||
Db         793 GACCGGGAAAAAGTGGTCGCCTTGTTTCAGGAGCTCGGATTCCAGTCGTTTCTCGACAAG 852

Qy         255 LeuArgAlaGlnIleAspGlu---------------------------------ThrLeu 263
               :::      |||   ||||||
Db         853 ATGGCCGTCCAAACGGATGAAGGCGAAAAGCCGCTCGCCGGGATGGATTTTGCGATCGCC 912

Qy         264 GluGluIleThrProArgTyrValLeuGluLeuLeuGlyLeu---------ProLeuGly 280
               :::   :::|||         :::   :::         |||            :::|||
Db         913 GACAGCGTCACGGACGAAATGCTCGCCGACAAAGCGGCCCTCGTCGTGGAGGTGGTGGGC 972

Qy         281 AspAspTyr-AlaAlaLysArgLeuAsnGlyLeuSerGlyValArgAsnIleLeuTrpSe 300
               |||:::|||          ||||||:::|||                        |||
Db         973 GACAACTATCACCATGCCCCGATTGTCGGGATCGCCT------------------TGGCC 1014

Qy         300 rValGlyGlyGlyGlyAlaSer-AlaLeuValGlyGlyLeuThrArgGluLysPheMetA 320
                         ||||||   ||| |||         |||      |||   :::
Db        1015 AACGAACGCGGGCGGTTTTTCCTGCGCCCGGAGACGGCGCTCGCCGATCCGAAATTTCTC 1074

Qy         320 snGluAlaPhe------------------------------------------------- 323
                    |||:::
Db        1075 GCTTGGCTTGGCGATGAGACGAAGAAAAAAACGATGTTTGATTCAAAGCGGGCGGCCGTC 1134

Qy         324 --------------LeuArgMetThrAlaAlaGluGlnVal-AspLeuPheValAlaThr 338
                                      ||||||      :::||| ||||||   :::|||
Db        1135 GCGCTAAAATGGAAAGGAATCGAACTGCGCGGCGTCGTGTTCGATCTGTTGCTGGCCGCT 1194

Qy         339 ProSerAsnIleProAlaGluSer---------------------PheGluValTyrGlu 351
                           ||||||::::::                        ::::::::::::
Db        1195 TACTTGCTCGATCCGGCGCAGGCGGCGGGCGACGTTGCCGCGGTGGCGAAAATGCATCAG 1254

Qy         352 ValAlaLeuAlaLeuValAlaGlnAlaPheIleGlyLys--------------------- 364
                                    :::|||      ||||||
Db        1255 TACGAGGCGGTGCGATCGGATGAGGCGGTCTATGGAAAAGGAGCGAAGCGGACGGTTCCT 1314

Qy         365 ---LysProHisLeuLeuGlnAspAlaAspLysGlnPheGlnGlnLeuGlnGlnAlaLys 383
                  :::|||   |||   :::         :::               :::   |||
Db        1315 GATGAACCGACGCTTGCCGAGCATCTCGCCCGC---------------AAGGCGGCGGCC 1359

Qy         384 ValMetAlaMetGluIleProAlaMetLeuTyrAspThrArgAsnAsnTrpGlu---Ile 402
               :::   |||:::|||   |||   |||            ||||||      :::   :::
Db        1360 ATTTGGGCGCTTGAAGAGCCGTTGATGGACGAACTGCGCCGCAACGAACAAGATCGGCTG 1419

Qy         403 AspPheGlyLeuGluArgGlyLeuCysAlaLeuLeuIleGly------------------ 416
                        ||||||:::   |||      :::|||
Db        1420 CTGACCGAGCTCGAACAGCCGCTGGCTGGCATTTTGGCCAATATGGAATTTACTGGAGTG 1479

Qy         417 LysValAspGluCysArgMet---TrpLeuGlyLeuAsp---SerGluAspSerGlnTyr 434
               |||||||||      |||:::      :::|||   :::   :::|||      |||
Db        1480 AAAGTGGACACGAAGCGGCTTGAACAGATGGGGGCGGAGCTCACCGAGCAGCTGCAG--- 1536

Qy         435 ArgAsnProAlaIleValGluPheValLeuGluAsnSerAsnArgAspAspAsnAspAsp 454
                        |||:::         :::   |||   :::   ::::::   |||   :::
Db        1537 ---------GCGGTCGAGCGGCGCATTTACGAACTCGCCGGCCAAGAGTTCAACATTAAC 1587

Qy         455 LeuProGlyLeuCysLysLeuLeuGluThrTrpLeuAlaGlyValValPheProArgPhe 474
                  |||         |||   |||   |||            |||:::|||   :::
Db        1588 TCGCCG---------AAACAGCTCGGGACG------------GTTTTATTTGACAAGCTG 1626

Qy         475 ArgAspThrLysAspLysLysPheLysLeuGlyAspTyrTyrAspAspProMetValLeu 494
               :::            ||||||   |||   |||   |||               ||||||
Db        1627 CAGCTCCCGGTGTTGAAAAAGACAAAAACCGGC---TATTCGACTTCAGCCGATGTGCTT 1683

Qy         495 SerTyrLeu---GluArgValGluValValGlnGlySerProLeuAlaAlaAlaAlaThr 513
                     |||            |||:::|||:::         :::
Db        1684 GAGAAGCTTGCACCGCACCATGAAATCGTCGAA------CATATTTTGCATTACCGCCAA 1737

Qy         514 MetAlaArgIleGlyAlaGluHisValLysAlaSerAlaMetGlnAlaLeuGlnLysVal 533
               :::   ::::::   :::   :::::::::         ::::::   :::      |||
Db        1738 CTCGGCAAGCTGCAGTCAACGTATATTGAA---GGGCTGCTGAAAGTGGTGCACCCCGTG 1794

Qy         534 PheProSerArgTyrThrAspArgAsnSerAlaGluProLysAspValGlnGluThr--- 552
                           :::|||      |||   |||            :::   :::|||
Db        1795 ACGGGCAAAGTGCACACGATGTTCAATCAGGCG------------TTGACGCAAACCGGG 1842

Qy         553 ---ValPheSerValAspProValGlyAsnAsnValGlyArgAspGlyGluProGlyVal 571
                  :::   ||||||:::|||         |||:::            |||   |||
Db        1843 CGCCTCAGCTCCGTCGAACCGAATTTGCAAAACATTCCGATTCGGCTTGAGGAAGGGCGG 1902

Qy         572 PheIleAlaGluAlaValArgProSerGlu------------------------AsnPhe 583
                  |||   :::|||      |||||||||                        ::::::
Db        1903 AAAATCCGCCAGGCGTTCGTGCCGTCGGAGCCGGACTGGCTCATCTTTGCGGCCGACTAT 1962

Qy         584 GluThrAsnAspTyrAlaIleArgAlaGlyValSerGluSerSerValAspGluThrThr 603
                        :::      :::   |||   ::::::|||         |||:::
Db        1963 TCGCAAATCGAGCTGCGCGTCCTCGCCCATATCGCGGAA---------GATGACAATTTG 2013

Qy         604 ValGlu---------------------------------------MetSerValAlaAsp 610
               :::|||                                       |||   :::
Db        2014 ATTGAAGCGTTCCGGCGCGGGTTGGACATCCATACGAAAACAGCCATGGACATTTTCCAT 2073

Qy         611 MetLeuLysGlu---------AlaSerValLysIleLeuAlaAlaGlyValAlaIleGly 627
               :::   :::|||         |||:::::::::      |||      |||      |||
Db        2074 GTGAGCGAAGAAGACGTGACAGCCAACATGCGCCGCCAAGCGAAGGCCGTCAATTTTGGC 2133

Qy         628 LeuIleSerLeuPheSerGlnLysTyrPheLeuLysSerSerSerSerPheGlnArgLys 647
               ::::::         |||      |||   |||      :::   :::      ||||||
Db        2134 ATCGTGTACGGCATTAGTGAT---TACGGTCTGGCGCAAAACTTGAACATTACGCGCAAA 2190

Qy         648 AspMetValSerSerMetGluSerAspValAlaThrIleGlySerValArgAlaAspAsp 667
               :::            :::|||         |||:::         |||:::
Db        2191 GAAGCGGCTGAATTTATTGAGCGATATTTTGCCAGTTTTCCAGGTGTAAAG--------- 2241

Qy         668 SerGluAlaLeuProArgMetAspAlaArgThrAlaGluAsnIleValSerLysTrpGln 687
                                          :::      :::|||||||||   :::
Db        2242 ---------------------------CAATATATGGACAACATTGTGCAAGAA---GCG 2271

Qy         688 LysIleLysSerLeuAlaPheGlyProAspHisArgIleGluMetLeuProGluValLeu 707
               |||   |||                     ||||||         ||||||::::::
Db        2272 AAACAAAAAGGGTATGTGACGACGCTGCTGCATCGGCGCCGCTATTTGCCCGATATTACA 2331

Qy         708 AspGlyArgMet---LeuLysIleTrpThrAspArgAlaAla---GluThrAlaGlnLeu 725
                              ::::::   :::   :::|||   |||      |||
Db        2332 AGCCGCAACTTCAACGTCCGCAGCTTCGCCGAGCGGACGGCGATGAACACACCGATCCAA 2391

Qy         726 GlyLeuValTyrAspTyrThrLeuLeuLysLeuSerValAsp---SerValThrValSer 744
               |||         |||      :::   |||      :::|||   ||||||   :::
Db        2392 GGGAGTGCCGCTGAT---ATTATTAAAAAAGCGATGATCGATCTAAGCGTGAGGCTGCGC 2448

Qy         745 AlaAspGlyThrArgAla------------------------------LeuValGluAla 754
                  :::      :::|||                              ::::::||||||
Db        2449 GAAGAACGGCTGCAGGCGCGCCTGTTGCTGCAAGTGCATGACGAACTCATTTTGGAGGCG 2508

Qy         755 ThrLeuGluGluSerAlaCysLeuSerAspLeuValHisProGlu 769
                     ||||||         |||      ||||||   ||||||
Db        2509 CCGAAAGAGGAAATCGAGCGGCTGTGCCGCCTCGTT---CCAGAG 2550

RESULT 10
US-08-436-664-21
; Sequence 21, Application US/08436664
; Patent No. 5874282
;  GENERAL INFORMATION:
;    APPLICANT:  RIGGS, MICHAEL G.
;    APPLICANT:  SIVARAM, MATHOOR
;    APPLICANT:  TUDOR, STARLA D.
;    TITLE OF INVENTION:  PURIFED DNA POLYMERASE FROM BACILLUS
;    TITLE OF INVENTION:  STEAROTHERMOPHILUS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gen-Probe Incorporated
;      STREET:  9880 Campus Point Drive
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92121
```

```
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: DOS
  SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/436,664
  FILING DATE: 08-MAY-1995
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/394,232
  FILING DATE:
  APPLICATION NUMBER: 08/307,410
  FILING DATE: 16-SEP-1994
  APPLICATION NUMBER: 08/222,612
  FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Fisher, Carlos A
  REGISTRATION NUMBER: 36,510
  REFERENCE/DOCKET NUMBER: GP94003.CP2
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 619-535-2807
  TELEFAX: 619-546-7929
  TELEX:
INFORMATION FOR SEQ ID NO: 21:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2631 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  FRAGMENT TYPE:
  ORIGINAL SOURCE:
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..2628
  OTHER INFORMATION:
US-08-436-664-21
```

```
Alignment Scores:
Pred. No.:
Score:                     0.000323
Percent Similarity:        134.50
Best Local Similarity:     37.1%
Query Match:               21.5%
DB:                        3.3%
                           2
```

```
Length:          2631
Matches:         194
Conservative:    141
Mismatches:      357
Indels:          212
Gaps:            45
```

US-10-600-070B-2 (1-801) x US-08-436-664-21 (1-2631)

```
Qy   398  AsnAsnTrpGlu---IleAspPheGlyLeuGlyArgGlyLeuCysAlaLeuLeuIleGly  416
               |||
Db  1402  AACGAACAAGATCGGCTGCTGCAACACCCCTGCTGCTGGCCATTTGG------------  1461

Qy   417  --------------LysValAspGluCysArgMet---TrpLeuGlyLeuAsp---     428
                        ||| :::            ::::                 |||
Db  1462  ATGGAATTTACTGGAGTGAGAGGTAGAAGTGGAGCGGCTTGAACAGATGGGGGCGGAGCTC  1521

Qy   429  SerGluAspSerGlnTyrArgAsnProLaIleValGluPheValLeuGluAsnSerAsn    448
               |||     :::                  :::
Db  1522  ACCGAGCAGCTGCAG------GCGGTCGAGGGCGGGCATTACGAACTGCCGGC         1569

Qy   449  ArgAspAspAspAsnAspAspLeuProGlyLeuCysGlyLysLeuLeuGluThrTrpProLeuLeuAlaGly  468
          :::::                           :::                        |||
Db  1570  CAAGAGTTCAACATTAACTCGCCG----------AAACAGCTCCGGACG             1608

Qy   469  ValValPheProArgPheArgAspThrLysGlyLysGlyPheLysGluGlyAspTyrTyr  488
          |||::         :::                  :::               |||
Db  1609  GTTTTATTTGAATTTGACAGCTCCAGCTCCCGGGTTGAAAAAGACAAAAACCGGC------TATTCG  1665

Qy   489  AspAspAspProMetValLeuSerTyrLeu---GluArgValGluValGlnGlySerPro  507
          |||                  :::                  :::
Db  1666  ACTTCAGCCGATGTGCTTGAGGAACGTTCGACCGACCACCGAAATCGTCGAA------CAT  1719

Qy   508  LeuAlaAlaLaAlaThrMetAlaAlaArgIleGlyAlaGluHisHisValLysSerAlaMet  527
                :::            :::                  :::
Db  1720  ATTTTGCATTACCGCCAACTCCGCCAAGCTGCACGTCAACGTATATTGAA--GGGCTGCTG  1776

Qy   528  GlnAlaLeuGlnLysValPheProSerArgTyrThrProAspArgAsnSerAlaGluProLys  547
                        ::::||                  :::
Db  1777  AAAGTGGGTGCACCCGTGACGGGCAAAGTGCACACGACGTTCAATCAGGCG           1827

Qy   548  AspValGlnGluThr------ValPheSerValAspProValGlyAsnAsnValGlyArg  565
                            :::                  :::
Db  1828  ---TTGACCCAAACCGGGGCGCCCTGCAGCTCCGTCGAACCCGAATTTGCAAAACATTCCGGATT  1884

Qy   566  AspGlyGluProGlyValPheIleAlaGluAlaValArgProSerGlu-----------  581
          |||                  :::                  :::
Db  1885  CGGCTTGAGGAAGGGCGGGAAAATCCGCCAGGGCGTTCGTGCGCCGGGACTGGCTC      1944

Qy   582  ------------AsnPheGluThrAsnAspTyrAlaIleLeuArgAlaGlyValSerGluSer  597
                      :::::                  :::::||
Db  1945  ATCTTTGCGGCCGGACTATTCGCAAATCGAGCTGTGGGCGTCCTCGCCCATATCGCCGGAA  2001

Qy   598  SerValAspGluThrThrValGlu------------                           605
          ::::                  :::
Db  2002  -----GAAGACAAATTTGATTGAAGGCGTTCCGGGGGGGCGGTTGGACATCATACGAAAACA  2055

Qy   606  --MetSerValAlaAspMetLeuLysGlu------------AlaSerValLysIleLeuAla  621
               |||                  :::                  ||| :::
Db  2056  GCCCATGGACATTTTCCATGTGAGGAGAAGAGACGTGACAGCCAACATGGCCGCCCGCCAAGCG  2115

Qy   622  AlaGlyValValAlaIleLeuIleSerLeuPheSerGlnLysTyrPheLeuLysSerSer  641
                        |||                  :::
Db  2116  AAGGCCGTCAATTTTGGCATGCGTCTACGGCCATTAGTGAT---TACGGTCTGGCCGCCAAAC  2172

Qy   642  SerSerPheGlnArgLysAspMetValSerSerMetGluSerAspValAlaLaThrIleGly  661
               :::                  :::                  |||
Db  2173  TTGAACATTACGGCCGCAAAGAAGGCGCTGAATTTATTGAGCGGATATTTTGCCAGTTTTCCA  2232

Qy   662  SerValArgGlyAlaAspAspSerGluAlaLeuProArgMetAspAlaArgThrAlaGluAsn  681
          |||:::            :::
Db  2233  GGTGTAAAG------------CAATATATGGACAAC                             2256

Qy   682  IleLeuValSerLysTrpGlnLysIleLysLysSerLeuAlaPheGlyProAspHisArgIleGlu  701
          |||:::            |||                  :::
Db  2257  ATGTGTCAAGAA------GCCAAACAAAAAGGGTATGTGACGACGTGCTGCATCCGGCCGCC  2313

Qy   702  MetLeuProGluValLeuLeuAspProAlaArgMet------LeuLysIleTrpThrAspProArgAlaAla  720
          |||:::::                  :::
Db  2314  TATTTGCCGGATAATTACAAGCCCGCAACTTCAACGTCCCGGCAGTTCGCCGAGCGCGACGGCG  2373

Qy   721  ---GluThrAlaGlnLeuGlnLeuValThrTyrAspTyrThrLeuLeuLysLeuSerValAsp  739
             |||                  :::                  :::
Db  2374  ATGAACAACACCGATCCAAGGGAGTGCCGCTGAT---ATTATTAAAAAAGGCGATGATCGAT  2430

Qy   740  ---SerValThrValSerGlrAlaAspGlyThrArgAla------                  750
             |||                  :::
Db  2431  CTAACGTCGAGGCGTCGCGCAAGAACGACGGCTGCAGGGGCGCCGGCTCTTGCTGCTTGCAAGTGCATGAC  2490

Qy   751  ------LeuValGlyGluAlaThrLeuGluGluSerAlaCysSerLeuSerAspLeuValHisPro  768
                :::::                  ||||||
Db  2491  GAACTCATTTTGGAGGGCGCCGAAAAGAAAGGAAAATCGAGCGGCGCCTTCGTT---CCA  2547

Qy   769  Glu                                                            769
          |||
Db  2548  GAG                                                            2550
```

US-08-436-664-31

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:

0.000323	
134.50	Length: 2631
37.1%	Matches: 194
21.5%	Conservative: 141
3.3%	Mismatches: 357
2	Indels: 212
	Gaps: 45

DB:

US-10-600-070B-2 (1-801) x US-08-436-664-31 (1-2631)

```
Qy    12 SerProPheGlnLeuCysArgLeuProProAlaThrThrLysLeuArgSerHisAsn 31
          :::||||||||
Db    47 GCGCCTTTTTCCGGTTGCCGCCTTTGCATAACGATAAAGGGATTCATACGACCAGTCT 106
```

```
Qy    32 ThrSerThrThrIleCysSerAlaSerLysTrpAlaSerAspPheAsn 51
          |||
Db   107 ACGGGTTTACGGATGATGTTAAACAAAATTTGCGGAAGAGCAGCCGACCCACATTCTCG 166
```

```
Qy    52 PheThrSerAspSerSerSerSerPheAlaThrAlaThr 65
          :::
Db   167 TGGCGTTT-GACCCGGGAAAACGACGTTCCAAGACTTTAAAGC 225
```

```
Qy    66 -----------ThrThrAlaThrLeuValSerLeuProProSerIleAspArgProGlu 81
          :::
Db   226 GGGCGCGGCAGCAGACGCGCCCCGGAACTGTCGGACAGTTTCCGCTGCTGCGGAATTGCTC 285
```

```
Qy    82 ArgHisValProIleProIleAspPheTyrGlnValLeuGlyLeuAlaGlnThrHisPheLeu 101
          :::
Db   286 AAGGGGTACCGGCATCCCCGCC------TATGACTC 332
```

```
Qy   102 ThrAspGlyIleArgArgAlaAlaPheGluAlaArgValSerLysProProGlnPheGlyPhe 121
          |||   |||
Db   328 GCGGACGATATTATCGGACGAGATGGCCGCCGGGCGGGCCTGGCCGACGAGAA 378
```

```
Qy   122 SerAspAlaAspAlaIleLeuSerArgArgGlnIleIleLeuLeuGlnAlaAlaCysGluThrLeuSer 141
          :::
Db   398 GCAGTGAAAGTCATTTCCGGACGACCGGCGATTTAACCAG--- 423
```

```
Qy   142 AsnProArgSerArgArgGluTyr---AsnGluGlyLeuLeuAsnAspGluAlaThr 160
          ::||||||  |||
Db   424 TCCCCGCAAGTGACACGGTGGGAGGAATTACGAAAAAAAGGGATTACCGACATCGGAGTCGGTACACG 483
```

```
Qy   161 ValIleThrAspVal------ 165
          |||
Db   484 CCGGAGACGGTCGTTGGAAAAATACGGGCCTCACCCCGGACGACAAATTGTCGACTTGAAAGGA 543
```

```
Qy   166 -----------ProTrpThrAspLysValProGly 173
          :::
Db   544 TTGGATGGGCGACAAAATCCCAACACATCCCTGGCGTGGCCCCGGCATCGGGGAAAAACAGC 603
```

```
Qy   174 LeuCysValLeuGlnLeuGlyLeuGlyValLeuLeuLeuLeuArgValGlyValAlaLeu 193
          :::
Db   604 GTCAAGCTTGCTCAAGCAATTCGCGACCGTCGAAAACGTACTGGCATCGATCGAGAGATC 663
```

```
Qy   194 LeuLysGluArgLeuProLysSerPheLysGln-------AspValLeuValMetAla 211
          |||
Db   664 AAAGGGGGAGAAGCTGAAAGAAAATTTGCCCAATACCGGGATTTGGCGGTT---TTAAGC 720
```

```
Qy   212 LeuAlaPheLeuAspValSerArgAspAla--------MetAlaLeuAspProProAsp 228
          :::
Db   721 AAACAGCTGGCCGCGTATTTCCGCGACGCCCCGGTTGACGCTCGAT--GAC 774
```

```
Qy   229 PheIleThrGlyTyrGluProPheValGlnGluGlyValGlnGluGlyAla 248
          :::
Db   775 ATTGTCTACAAAGGAGAGAAGAGCCCGGAAAAAGTGCGGCTTGTTCAGGAGCTCGGATC 834
```

```
Qy   249 SerSerLeuAlaProAspLeuArgAlaGlnIleAspGlu----- 261
          |||
Db   835 CAGTCGTTTTCGACAAGAGGGCCGTTCCAAAACGCGGCTCGCCCGGG 894
```

```
Qy   262 ------ThrLeuGluGluIleThrProArgTyrValLeuGluLeuLeuGlyLeu 277
```

```
Db   895 ATGGGATTTTGCGATCGCGCCGACACCGTCACGGACGGAAATGCTCGCCGACAAAGCCGCCCTC 954
          :::  |||
```

```
Qy   278 -----ProLeuGlyAspAspTyr-AlaAlaLysArgLeuAsnGlyLeuSerGlyVa 294
          :::||||||::::||
Db   955 GTCCTGGAGGTGGTGGTCGGGGCGGACAACTATCACCATGCGCGGAAGAAAGATGTTTGAT 1009
```

```
Qy   294 lArgAsnIleLeuTrpSerValGlyGlyGlyAlaSer-AlaLeuValGlyGlyLeuThr 314
          |||::::|||
Db  1010 TGGCCAACGAACGCGCGGGCGCGGGGGTTTTCCTCGCGCTCGCCCGGAGGACGGGCTC 1056
```

```
Qy   314 hrArgGluLysPheMetAsnGluAlaPhe--------------- 323
          :::
Db  1057 GCCGATCCGAAAATTTCTCGCCTTGGCCTTGGCGATGAGAGAGAAAAACGATGTTTGAT 1116
```

```
Qy   324 -----------LeuArgMetThrAlaAlaGluGlnVal- 332
          |||
Db  1117 TCAAAGCGCGGGGCGCGGCCGTCGCGCTAAAATGGAAAGGAAATCGACTGCGCCGGGGG 1176
```

```
Qy   333 AspLeuPheValAlaLeuThrProSerAsnIleProAlaGluSer----------- 346
          |||::::|||::::::::
Db  1177 GATCTTGTTGCGCTGCTGCGGCCGCTTACTTGCTCGATCCGGGAATCCCGGCGGAGTCG 1236
```

```
Qy   347 ---PheGluValTyrGluValAlaLeuValAlaLeuValAlaLeuAlaPheIleGlyGlyLys-- 364
          :::
Db  1237 GTGGCGAAAAATGCATCAGTTACGGACGGCGGTGCGATCGGATGAGGCGGGTCTATGGAAAAGGA 1296
```

```
Qy   365 -----------LysProHisLeuLeuGlnIleAspAlaAspGlyGlnPheGln 377
          :::
Db  1297 GCGGAAGCGGACGGTTCCGGATGAACCGACGCTTGCGGCATCCGCCGC----- 1347
```

```
Qy   378 GlnLeuGlnLeuAlaLysValMetAlaMetGluTleProAlaMetLeuTyrAspThrArg 397
          :::|||::::|||
Db  1348 -----AAGGCGGGCGGCCATTTGGGCGCGTTGAAGAGCCGCGG 1401
```

```
Qy   398 AsnAsnTrpGlu-----IleAspPheLeuGlyLeuAspLeuCysLeuCysAlaLeuLeuIleGly 416
          :::
Db  1402 AACGAACAAGATCGGCTACTTGACCGGAGCTCGAACAGCCCGCTGGCTGGCATTTGGCCAAT 1461
```

```
Qy   417 -----LysValAspGluCysArgMet---TrpLeuGlyLeuAsp- 428
          :::
Db  1462 ATGGAAAATTTACTGGAGTGAGATGGACACGAAGCGGGCTTGAACAGATGGGGCGAGCTC 1521
```

```
Qy   429 SerGluAspSerGlnTyrArgAsnProAlaIleValGluLeuGluAsnSerAsn 448
          :::|||
Db  1522 ACCGAGCAGCTGCAG-----GCGGTCGAGGCGGGCCATTACGAACTCGCCGGC 1569
```

```
Qy   449 ArgAspAspAsnAspAspLeuProGlyLeuCysLysLeuLeuGluThrTrpLeuAlaGly 468
          :::
Db  1570 CAAGAGTTCAACATTAACTCGCG----AAACAGCTCGGCGACG 1608
```

```
Qy   469 ValValPheProArgPheArgAspThrLysPheLysGlyAspTyrTyr 488
          |||:::|||
Db  1609 GTTTTATTTGACAACAGCTCCCGGGTGTTGAAAAGACAAAAACCGGC---TATTCG 1665
```

```
Qy   489 AspAspProMetValLeuSerTyrLeu---GluArgValGlnValGlnGlySerPro 507
          |||::::|||
Db  1666 ACTTCAGCCGATGTCCTTGAGAAGGTTGCACCGACCATAGAAATCGTCGAA---CAT 1719
```

```
Qy   508 LeuAlaAlaAlaThrMetAlaArgIleLeuGlyAlaGluHisValLysValAlaSerAlaMet 527
          :::
Db  1720 ATTTTGCATTACCGGCAACTCGCAAGCTGCCAGTCAACGTATATTGAA---GGGCTGCTG 1776
```

```
Qy   528 GlnAlaLeuGlnLeuValPheProSerArgTyrThrArgAspArgAsnSerAlaGluProLys 547
          :::
Db  1777 AAAGTGGGTGGCACCCCGTGACGGGCGAAAGTGCACAACGGATGTTCAATCAGGCG----- 1827
```

```
Qy   548 AspValGlnGluThr-------ValPheSerValAspProValGlyValAsnAsnValGlyArg 565
          :::
Db  1828 ---TTGACGCAAACCGGCGCGCCCTCAGCTCCGTCGGACGGAATTTGCAAAAAACATTCGGATT 1884
```

```
Qy   566 AspGlyGluProGlyValPheIleAlaGluAlaValArgProSerGlu----------- 581
          |||   :::|||
```

```
Db 1885 CGGCTTGACGAGGGGCGGAAAATCCGCCAGGGCGTTCGTCGTCCGGTCGGGAGCCGGACTGGGCTC 1944
                                ::|                   |::|   |||
Qy  582 ------------AsnPheGluThrAsnAspTyrAlaIleArgAlaGlyValSerGluSer 597
Db 1945 ATCTTTGCGGGCCGACTATTCGCAAATCAGAGCTCGCGGGGTCCTCGCCCATATCGCCGAA--- 2001

Qy  598 SerValAspGlyThrThrValGlu--------------------------------- 605
         |||       ::|:            |||
Db 2002 -----GATGACAATTTGATTGAAGCGTTCCGGGCGGGGGGTTGGGACATCCATACGAAAACA 2055

Qy  606 ---MetSerValAlaAspMetLeuLysGlu----------AlaSerValLysIleLeuAla 621
          :::                            :|:|:|   |:|
Db 2056 GCCATGACAGTTTTCCAGTGACGGAAGAAGAGACCGTGACAGCCCAACATCGCCCAAGCG 2115

Qy  622 AlaGlyValAlaIleGlyLeuIleSerLeuPheSerGlnLysTyrPheLeuLySerSer 641
                   |||               :::               |||
Db 2116 AAGGCCGTCAATTTTGGCATCGTCGTACGGCCATTAGTTGAT---TACGGTCTGGCGCAAAC 2172

Qy  642 SerSerPheGlnArgLysAspMetValSerSerMetGluSerAspValAlaThrIleGly 661
          |||:::                                            |||
Db 2173 TTGAACATTACGGCGCAAAGAAGCCGCTGAATTTATTGACGGATATTTTCCCAGTTTTCCA 2232

Qy  662 SerValArgAlaAspAspSerGlyValAlaLeuProArgMetAspAlaArgThrAlaGluAsn 681
                  :::                                        |||
Db 2233 GGTGTAAAG---------------------------CAATATATGGGACAAC 2256

Qy  682 IleValSerLysTrpGlnLysLysIleLeuLysGlySerLeuAlaPheGlyProAspHisArgIleGlu 701
         ||||||                                        |||:::
Db 2257 ATTGTGCAAGAA---GCGAACAAAAAGGGTATGTGACGACGTGCTGACATCCGCGCCC 2313

Qy  702 MetLeuProGluValLeuValAspGlyArgMet---LeuLysIleTrpThrThrAspArgAlaAlaAla 720
          :::|||::::                        ::::||||||
Db 2314 TATTTGCCCGATATTACAGACCGGAACTTCAACCGTCCGCCGAGCCGACGGGCG 2373

Qy  721 ---GluThrAlaGlnLeuGlyLeuValTyrAspTyrThrLeuLeuLysSerValAsp 739
            |||                                       |||:::
Db 2374 ATGAACACACCGACATCCAAGGGACTGCCCCTGAT---ATTATTAAAAAAGCGATGATCGAT 2430

Qy  740 ---SerValThrValSerArgAlaAspGlyThrArgAla--------- 750
           |||:::                           |||:::
Db 2431 CTAAGGCGTTGAGCGCTGCCGGAGAACCGGCGTCCAGGCGCGCGCCCGTTGCTCGAAGTGCATGAC 2490

Qy  751 ------LeuValGluAlaThrLeuGluGluSerAlaCysLeuSerAspLeuValHisPro 768
               :::|||||                           |||
Db 2491 GAACTCATTTTGGAGGCGCCGAAAAGAGAGAAATCGAGCGGCCCTGTGCGCGCCTCGTT---CCA 2547

Qy  769 Glu 769
        |||
Db 2548 GAG 2550
```

```
RESULT 12
US-09-135-642-21
Sequence 21, Application US/09135642
Patent No. 606483

Alignment Scores:
Pred. No.:
Score:                      0.000323
                          134.50
Percent Similarity:        37.1%
Best Local Similarity:     21.5%
Query Match:               3.3%
DB:

Length:         2631
Matches:         194
Conservative:    141
Mismatches:      357
Indels:          212
Gaps:             45
```

US-10-600-070B-2 (1-801) x US-09-135-642-21 (1-2631)

```
Qy   12 SerProPheGlnLeuCysArgLeuProProAlaThrThrLysLeuArgSerHisAsn 31
         ::||||||||      ||      ||   |||:::
Db   47 GCGCCTTTTCGCGTTGCCGCTTTGCAGTAACGATAAAGGGATTCATACGAGAACGCAGTCT 106

Qy   32 ThrSerThrThrIleCysSerAlaSerLysTrpAlaAspArgLeuLeuSerAspPheAsn 51
         |||                ||      |||:::
Db  107 ACGGGTTTACGATGAGATTGTTAAACAAAATTTTGGCGGAAGAGCAGCCGACCCACATTCTCG-166

Qy   52 PheThrSerAspSerSerSerSerSerPheAlaThrAlaThr--------- 65
          |||:::                               |||
Db  167 TGGCGTTT-GACGGCCGGGAAAACGACGTTCCGCCATGAAACGTTCCAAGACTATAAAGGC 225

Qy   66 --------ThrThrAlaThrLeuValSerLeuProProSerIleAspArgProGlu 81
                 |||               |||:::
Db  226 GGGCGGGCCAGCAGACGCCCGCCGGACTGTCCGACACAGTTTCCGCTGCGGGAATTGCTC 285

Qy   82 ArgHisValProIleProIleAspPheTyrGlnValLeuGlyAlaGlnThrHisPheLeu 101
          |||:::                                     |||
Db  286 AAGGCGTACCGATCGCATCCCCCGCC-----TATGAGCTC---------GACCATTACGAA 327

Qy  102 ThrAspGlyIleArgArgAlaPheGluAlaValSerLysProGlnProPheGlyPhe 121
          |||                  |||                      |||:::
Db  328 GCGGACGGATATTACGGACACGGATCGGCGGGCGCTGAGCGAGAA------GGGTTT 378

Qy  122 SerAspAspAlaLeuIleLeuSerArgArgGlnIleLeuGlnAlaAlaCysGluThrLeuSer 141
          :::                               |||:::
Db  379 GCAGTGAAAGTCATTCCGGCGACGGCCGATTAACCCAG-----CTTGCT 423
```

```
Db      2431 CTAAGCGTGAGGCGTGCGCGAAGAAGCGGCTGCGACGGCGGGCCGCCTGTTGCTGGAAGTGCATGAC 2490
             |||||         :::         |||
Qy       751 -----LeuValGluLeuThrLeuGluGluSerAlaCysLeuSerAspLeuValHisPro 768

Db      2491 GAACTCATTTTGGAGGCGCCGAAAGAGAGAAATCGAGCGCGTGCCGCGCCTCGTT---CCA 2547
             ::|::||||||||     ||||||           ||||||
Qy       769 Glu 769

Db      2548 GAG 2550
             |||
Qy       769 GAG 2550
```

RESULT 13
US-09-135-642-31
; Sequence 31, Application US/09135642
; Patent No. 6066483
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATHOOR
; APPLICANT: TUDOR, STARLA D.
; TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS
; TITLE OF INVENTION: STEAROTHERMOPHILUS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/394,232
; FILING DATE:
; APPLICATION NUMBER: 08/307,410
; FILING DATE: 16-SEP-1994
; APPLICATION NUMBER: 08/222,612
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94003.CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..2631
; OTHER INFORMATION:
US-09-135-642-31

```
Alignment Scores:
Score:             0.000323        Length:    2631
Pred. No.:         134.50          Matches:   194
```

```
Qy      769 Glu 769
            |||
Db     2548 GAG 2550
```

Percent Similarity: 37.1%   Conservative: 141
Best Local Similarity: 21.5%   Mismatches: 357
Query Match: 3.3%   Indels: 212
DB: Gaps: 45

US-10-600-070B-2 (1-801) x US-09-135-642-31 (1-2631)

```
Qy       12 SerProPheGlnLeuCysSerAlaSerLysTrpAlaAspArgLeuProProAlaThrThrLysLeuLeuSerAspPheAsn 51
            :::|||||||                |||||||||                                |||||:::
Db       47 GCGCCTTTTTTCGCGTTGCCGCTTTGCGCGTTGTTGCATAACGATAAAGGGATTCATCATCGGAATCAACCGAGTCT 106

Qy       32 ThrSerThrThrIleCysSerAlaSerLysTrpAlaAspArgLeuLeuSerAspPheAsn 51
            :::||||||||||                                  |||||:::
Db      107 ACGGGTTTACGATGATGTTAAACAAAATTTTGGGGAAGACGACCACATTCTCG 166

Qy       52 PheThrSerSerSerSerSerPheAlaThrAlaThr----------------------------- 65
            |||:::        ||||||:::
Db      167 TGGCGTTT-GACGCCCGGGAAAACGACGTTCCGCCATGAAACGTTTAAAGGC 225

Qy       66 ------------ThrThrAlaThrLeuValSerLeuProProSerIleAspArgProGlu 81
                        |||               :::
Db      226 GGGGCGGCAGCAGCACGCCGCCGGGACTGTCGGAACAGTTTCCGCTGCTGGGAATTGCTC 285

Qy       82 ArgHisValProIleProIleAspPheTyrGlnValLeuGlyAlaGlnThrHisPheLeu 101
            :::|||||||                    |||||:::
Db      286 AAGGCGTACCGCATCCCCGCC-----TATGAGCTC-----GACCATTACGAA 327

Qy      102 ThrAspGlyIleLeuArgArgAlaPheGluAlaArgValSerLysProProGlyPhe 121
            |||||||               |||||||||               :::
Db      328 GCGGACGGATATTACGGAACGATGGCGCCGCGGGCGCTGAGGGAGAA-----GGGTTT 378

Qy      122 SerAspAspAlaLeuLeuIleSerArgArgGlnIleLeuLeuGlnAlaAlaCysGluThrLeuSer 141
            |||:::        |||               :::        CTTGCT
Db      379 GCAGTGAAAGTCATTTCGCGCACCGCGATTTAACCCAG----------------------- 423

Qy      142 AsnProArgSerArgArgGluTyr---AsnGluGlyLeuLeuAspAspGluGlyAlaThr 160
            |||||||               :::|||:::               |||
Db      424 TCCCCGCGAAGTGACGGGTGGGAGTTACGGAAAAAAGGGATTACCGACATCGAGTCGTACACG 483

Qy      161 ValIleThrAspVal--------------------------------- 165
            |||
Db      484 CCGGAGACCGTCGTGGAAAAATACGGCCTCACCCCGGAGCAAATTGTCGGACTTGAAGGA 543

Qy      166 ---------ProTrpAspLysValProGly------------------------------Ala 173
                     |||:::        |||               :::        Ala
Db      544 TTGATGGGCGACAAAATCCGACAACATCCCTGGCGTCGCCCGGGATCGGGGGAAAAAACAGCC 603

Qy      174 LeuCysValLeuGlnLeuGlyGlyThrGluIleValLeuLeuLeuArgValGlyAlaLeu 193
            :::|||||||               :::        |||               :::
Db      604 GTCAAGCTGCTCAAGCAATTCGGCACGGGTCGGAAAAACGTACTGGCGATCGATCGAGATC 663

Qy      194 LeuLysGluArgLeuProLysSerPheLysGln-----AspValValLeuValMetAla 211
            |||||||               :::|||:::
Db      664 AAAGGGGAGAAGCTGAAAGAAAATTTGCCCAATACCCGGATTTGGCGCTT---TTAAGC 720

Qy      212 LeuAlaPheLeuAspValSerArgAspAla---------MetAlaLeuAspProProAsp 228
            |||:::        |||               :::        GAC
Db      721 AAACAGCTGGCCCCCTTATTTGCCCGGTTGAGCTGACGGCTCGAT-----GAC 774

Qy      229 PheIleThrGlyTyrGluPheValGluLeuLysLeuLeuGlnGluGluGlyAla 248
            |||:::        |||||||:::        |||
Db      775 ATTGTTCTACAAGGAGAAGAGACCGGGAAAAAGTGGTTCAGGAGCTCGGATTC 834

Qy      249 SerSerLeuAlaProAspLeuArgAlaGlnIleAspGlu----------------- 261
            |||               :::        |||
Db      835 CAGTCGTTTCTCGACACAAGATGGCCGTCCAAACCGATGAAAGGCCGCTCGCCGGG 894

Qy      262 ---------ThrLeuGluGluIleThrProArgTyrValLeuLeuIleLeuGlyLeu 277
            :::        |||               |||:::        |||
Db      895 ATGGATTTTTGCGATCGCGACCACGCGTCACGGACGAAAATGCTCCGCGACAAAGGGCCTC 954

Qy      278 -----------ProLeuGlyAspAspTyr-AlaAlaLysArgLeuAsnGlyLeuSerGlyVal 294
            :::|||:::        |||               |||:::        ||||||
Db      954
```

RESULT 14
US-08-394-232A-21
; Sequence 21, Application US/08394232A
; Patent No. 6100078
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATHOOR
; APPLICANT: TUDOR, STARLA D.
; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILIU
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; APPLICATION NUMBER: US/08/394,232A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/307,410

[Sequence alignment data — Query (Qy) and Database (Db) rows with nucleotide and translated amino acid sequences]

```
;  FILING DATE:  16-SEP-1994
;  APPLICATION NUMBER:  08/222,612
;  FILING DATE:  16-SEP-1994
;  ATTORNEY/AGENT INFORMATION:
;      NAME:  Fisher, Carlos A
;      REGISTRATION NUMBER:  36,510
;      REFERENCE/DOCKET NUMBER:  GP94003.CP2
;  TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-535-2807
;      TELEFAX:  619-546-7929
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  21:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH:  2631 base pairs
;          TYPE:  nucleic acid
;          STRANDEDNESS:  single
;          TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
;      HYPOTHETICAL:  NO
;      ANTI-SENSE:  NO
;      FRAGMENT TYPE:
;      ORIGINAL SOURCE:
;      FEATURE:
;          NAME/KEY:  Coding Sequence
;          LOCATION:  1..2628
;      OTHER INFORMATION:
US-08-394-232A-21

Alignment Scores:

Pred. No.:               0.000323
Score:                   134.50
Percent Similarity:      37.1%
Best Local Similarity:   21.5%
Query Match:             3.3%

DB:

             Length:     2631
             Matches:    194
             Conservative: 141
             Mismatches: 357
             Indels:     212
             Gaps:       45

US-10-600-070B-2 (1-801) x US-08-394-232A-21 (1-2631)
```

```
Qy      12  SerProPheGlnLeuCysArgLeuProProAlaThrThrLysArgSerHisAsn  31
            ::|||||||||
Db       1  GGCCCTTTTCCGTTGCCGCTTTGCATAAACGATAAAGGATTCATACGACCAGTCT 106

Qy      32  ThrSerThrThrIleCysSerAlaSerLysTrpAlaAspAlaArgLeuLeuSerArgAspPheAsn  51
            |||  :: ::|
Db     107  ACGGGTTTACGATGATGTTAAACAAAATTTTGCGAAGAGCAGCCACCCACATTCTCG 166

Qy      52  PheThrSerAspSerSerSerSerPheAlaThrAlaThr-  65
            ::::||||  :::
Db     167  TGGCGTTT-GACGCCCGGGAAAAACAGACTTCCCGCCATGAAAACGTTCCAAGACTATAAAGGC 225

Qy      66  ------------ThrThrAlaThrLeuValSerLeuProProSerIleAspArgProGlu  81
            |||  :::
Db     226  GGGCGGGGCAGACGCCCGCCGGAACTGTCGGAACAGTTTCCGCGGGAATTGCTC 285

Qy      82  ArgHisValProIleProIleAspPheTyrGlnValLeuGlyAlaGlnThrHisPheLeu 101
            :||||:::
Db     286  AAGGCGTTACCGCATCCCGCC------TATGAGCTC 327

Qy     102  ThrAspGlyIleArgArgAlaPheGluAlaArgValSerLysProProGlnPheGlyPhe 121
            |||
Db     328  GCGGACGGATATTATCCGGAACGATGGCGCGCGCCTGAGCGGAA 378

Qy     122  SerAspAspAlaLeuIleSerArgArgGlnIleLeuGlnIleAlaAlaCysGluThrLeuSer 141
            ::::
Db     379  GCAGTGAAAGTCATTTCCGCGGACCGGATTAAACCCAG------CTTGCT 423

Qy     142  AsnProAspSerArgArgArgGluTyr--AsnGluGlyLeuLeuAspAspGluValAlaThr 160
            :::
Db     424  TCCCCGCAAGTGACGGTGGAGATTACCGAACAAAAAGGGGATTACCGACATCGAGTCGTACACG 483

Qy     161  ValIleThrAspVal-  165
            |||
Db     484  CCGGACGACGGTCGTGGAAAAATACGGCCTCACCCCGAGCAAATTGTCGACTTGAAAGGA 543
```

```
Db     166  -----------ProTrpAspLysValProGly------------Ala 173
               |||  :::|||||  :::|||
Db     544  TTGATGGGGGGCAGAAATCCGACAACATCCCTGGCGCCGCCATCGGGGGAAAAAACAGCC 603

Qy     174  LeuCysValLeuGlnLeuGlnGlyLeuGluThrGluIleValLeuValArgValGlyAlaLeu 193.
               :::  :::|||
Db     604  GTCAAGCTGCTCAAGCAATTCGGCACGGTCGAAAAGGTTACTGGCATCGATGAGATC 663.

Qy     194  LeuLysGluArgGlyLeuProLysSerPheLysGln-----AspValValLeuValMetAla 211
            |||:::|||  :::|||
Db     664  AAAGGGGAGGAAGCTGAAAGAAAATTTGCGCCAATACCCGGCGGATTTGGCCGTT---TTAAGC 720

Qy     212  LeuAlaPheLeuAspValSerArgAspAla--------MetAlaLeuAspProProAsp 228
            :::|||  :::
Db     721  AAACAGCTGGCCGCTATTTGCCGCGACGCCCCCGGTTGAGCTGGCGCTCGAT-----GAC 774

Qy     229  PheIleThrGlyTyrGluPheValGluValGlyAlaLeuLysLeuLeuGlnGluGlnGlyAla 248
               :::|||
Db     775  ATTGTCTACAAAGGAGAAGACCGGGAAAAAGTGGGTCGGCTTGTTTCAGGAGCTCGGATTC 834

Qy     249  SerSerLeuAlaProAspLeuArgAlaLeuGlnIleIleAspGlu----------- 261
               |||
Db     835  CAGTCGTTTCTCGACAAGATGGCGTCCAAAACGATGAAAGGCCGCTCGCCGGG 894

Qy     262  -------------ThrLeuGluGluIleThrProArgTyrValLeuGluLeuGlyLeu 277
               :::|||  :::
Db     895  ATGGATTTTGCGATCGCGACACGTCACGGACGAAAATGCTCCGGACAAAAGCGGCCTC 954

Qy     278  -----------ProLeuGlyAspAspTyr-AlaAlaLysArgLeuAsnGlyLeuSerGlyVa 294
            :::|||  :::|||  :::|||
Db     955  GTCGTGGAGGTGGGTGGGCCGGACAACTATCACCATGCGGGATGCCT----1009

Qy     294  lArgAsnIleLeuTrpSerValGlyGlyGlyGlyAlaSer-AlaLeuValGlyGlyLeuT 314
               |||  :::
Db    1010  -TGGCCAACGAACGCGGCGGCGGTTTTTCGTGCCCGAGACGGGCGCTC 1056

Qy     314  hrArgGluLysPheMetAsnGluAlaPhe------------  323
            |||
Db    1057  GCGGATCCGAAAATTTCTCGGCTTGGCTTGGCGATGGAAGAAAAACGAGTTTGAT 1116

Qy     324  ------------LeuArgMetThrAlaAlaGluGlnVal- 332
               :::|||
Db    1117  TCAAAGCGGGGGGCGCGGTTCGGCGTCGGCCTAAAATGGAAAGGAACGTCGCGGGCGTCGGTTC 1176

Qy     333  AspLeuPheValAlaAlaThrProSerAsnIleProAlaGluSer------------  346
            |||  :::
Db    1177  GATCTGTTCGTCGCGCTTACTTCGTCCTCGAATCCCGCGCAGGCGGGTTGCCGCG 1236

Qy     347  --PheGluValTyrGluValAlaLeuLeuValAlaLeuGlnAlaPheIleGlyLys-- 364
            :::|||:::|||
Db    1237  GTGGCGAAAATGCATCAGTACGGAGGGGTGCGAACGGGGTCTATGGAAAAAGGA 1296

Qy     365  ------------LeuProHisLeuLeuGlnAspAlaAspLysGlnPheGln 377
               :::|||
Db    1297  GCGGAAGCGGACGGGTTCCTGATGAACCACGCCTTGCCGGACATCCGCCCGC------1347

Qy     378  GlnLeuGlnHisAlaLysValMetAlaMetGluIleProAlaMetLeuTyrAspThrArg 397
            |||  :::|||
Db    1348  -----AAGGCGCGGCCATTTGGGCGCGTTGAAGAGCCGTGATGGACCAACTCGCGCC 1401.

Qy     398  AsnAsnTrpGlu---IleAspPheGlyLeuArgGlyLeuCysAlaLeuLeuIleGly 416
            |||  :::
Db    1402  AACGAACAAGATCGGATCGCTGACCGAGCTGAAACAGCGGCCGCCATTTTGGCCAAT 1461

Qy     417  ------------LysValAspGluCysArgMet---TrpLeuGlyLeuAsp--- 428
            :::||||||
Db    1462  ATGGAAATTTACTGGAGTGAAAGTGGAACAACGAACGCCTTGAACAGATGGCGGGAGCTC 1521

Qy     429  SerGluAspSerGlnTyrArgAsnProAlaIleValGlyPheValLeuGluAsnSerAsn 448
            :::|||:::
Db    1522  ACCGAGCAGCTGCAG--------GCGGTCGAGCGCGCATTACGAACTCGCCGGC 1569
```

```
Qy   449 ArgAspAspAsnAspAlaProLeuCysLysLeuLeuGluThrTrpLeuAlaGly 468
         |||:||
Db  1570 CAAGAGTTCAACATTAACTCGCCG------AAACAGCTCGGGACG------ 1608

Qy   469 ValValPheProArgPheArgAspThrLysAlaLysPheLeuGlyAspTyrTyr 488
         |||:||     :::    |||
Db  1609 GTTTTATTTGACAAGCTGCAGCTCCCGGTGTTGAAAAAGAACAAAAACCGGC--TATTCG 1665

Qy   489 AspAspProMetValLeuSerTyrLeu--GluArgValGluValGlnGlySerPro 507
         :::          |||
Db  1666 ACTTCAGCCGGATGTGCTTGAGAAGCTTGACCGCACCCATGAAAATCGTCGAA-----CAT 1719

Qy   508 LeuAlaAlaAlaAlaThrMetAlaArgIleGlyValAlaGluHisValLysAlaSerAlaMet 527
         :::
Db  1720 ATTTTGCATTACCGCCAACTCGCAAGCTGCAGTCAACGTATATTGAA---GGGCTGCTG 1776

Qy   528 GlnAlaLeuGlnLysValPheProSerArgTyrThrAspArgAsnSerAlaGluProLys 547
Db  1777 AAAGTGGGTGCACCCGTGACGGGCGAAAGTGCACACGAATGTTCAATCAGGCG------- 1827

Qy   548 AspValGlnThr------ValPheSerValAspProValGlyAsnAsnValGlyArg 565
         :::        |||
Db  1828 ---TTGACGCAAACCGGGGCGCCTTCAGCTCCGTTGAACCGAATTGCAAAACAATTCCGATT 1884

Qy   566 AspGlyGluProGlyValPheIleAlaGluAlaValAlaValArgProSerGlu-- 581
         |||
Db  1885 CGGGCTTCGAGGAAGGGCCGAGAAAATCCGCCAGGGCGTTCGTGCCGTTCGGAGCCGGACTGGCTC 1944

Qy   582 ------AsnPheGluThrAsnAspTyrAlaIleGlyValAlaGlyValSerGluSer 597
         :::        |||
Db  1945 ATCTTTGCGGCGGACTAATCCGTGTTACGGGCATTAGTTGAT--- 2001

Qy   598 SerValAspGluThrThrValGlu------ 605
         :::|||
Db  2002 --GATGACAATTGAATTGAAGCGGTTCCGGCCGGGGGTTGGACATCCATACGAAAACA 2055

Qy   606 ---MetSerValAlaAspMetLeuLysGlu------AlaSerValLysIleLeuVa 621
         :::            |||
Db  2056 GCCATGACACATTTTCCAATGTGACGGAGAAGACGTGACAGCCAACATCGCCCGCCAAGCG 2115

Qy   622 AlaGlyIleValAlaIleGlyLeuIleSerLeuPheSerGlnLysTyrPheLeuLeuLysSerSer 641
         |||
Db  2116 AAGGCCGTCAATTTTGGCATCGTTGTACGGGCATTAGTTGAT---TACGGTCTGGCGCAAAAC 2172

Qy   642 SerSerPheGlnArgLysAspMetValSerSerMetGluSerAspValAlaThrIleGly 661
         :::              |||
Db  2173 TTGAACATTACGGCACAAAGAACGGCGGCTGAATTTATTGAGCGGATATTTTTTCCAGTTTTCCA 2232

Qy   662 SerValArgAlaAspAspSerGluAlaLeuProArgMetAspAlaArgThrAlaGluAsn 681
         :::
Db  2233 GGTGTAAAG--------------------CAATATATGGACAAC 2256

Qy   682 IleGluValSerLysTrpGlnLysIleLysSerLeuAlaPheGlyTyrProAspHisArgIleGlu 701
         |||        ||||||:|
Db  2257 ATTGTGCAAGA--GCGAAACAAAAAGGGTATGTGACGACGCGCTGCTCGGGCGGCCGC 2313

Qy   702 MetLeuProGluValLeuAspGlyArgMet---LeuLyssIleTrpThrAspArgArgAlaAla 720
         |||           :::|||:||||||
Db  2314 TATTTGCCCGGATAATTACAAGCCCGAACTTACGGCAGCTTGCCGCAGCCGGACGGCG 2373

Qy   721 ---GluThrAlaGlnInLeuGlyValValTyrAspTyrThrLeuLeuLysLeuSerValAsp 739
         :::              |||
Db  2374 ATGAACACACCGATCCCAAGGGAGTGCCCGCTGAT---ATTATTAAAAACGGATGATCGAT 2430

Qy   740 ---SerValThrValSerAlaAspGlyThrArgAla 750
         :::|||
Db  2431 CTAAGGCGGCTGCGCGGAAGAACGGCTCGCAGGCGGCCCTGTTGCGCTGCCGCCAAGTGCATGAC 2490

Qy   751 -----LeuValGluAlaThrLeuGluSerAlaCysSerAspLeuValHisPro 768
         :::|||||||||
Db  2491 GAACTCATTTTGGAGGCGGCGACGGAAAGAGGAAATCGAGCGGCGGCCTGTCGCCGCCTCGTT--CCA 2547

Qy   769 Glu 769
         |||
Db   769 Glu 769
```

Db   2548 GAG 2550
          |||

Alignment Scores:

Pred. No.:	0.000323
Score:	134.50
Percent Similarity:	37.1%
Best Local Similarity:	21.5%
Query Match:	3.3%
DB:	

Length:	2631
Matches:	194
Conservative:	141
Mismatches:	357
Indels:	212
Gaps:	45

US-10-600-070B-2 (1-801) x US-08-394-232A-31 (1-2631)

```
Qy   12 SerProPheGlnLeuCysArgLeuProProAlaThrThrLysLeuArgArgSerHisAsn 31
        :::||||||       |||:::
Db   47 GCGCCTTTTTGCGCGTTGCCGCTTTGCGATAACGATAAAAGGGGATTCATACGGAACGCAGTCT 106
```

```
Qy    32 ThrSerThrThrIleCysSerAlaSerLysTrpAlaAspArgLeuLeuSerAspPheAsn    51
         |||:::
Db   107 ACGGGTTTACGATGATGTTAAACAAAATTTTGGGGACAGAGCAGCCACATTCTCG       166

Qy    52 PheThrSerAspSerSerSerPheAlaThrAlaThr------                       65
         :::  ||||::||
Db   167 TGGCGTTT-GACCCCGGAGAAAACAGACGTTCCGCTGCCATGAAAACGTTTAAAGC       225

Qy    66 ------------ThrThrAlaThrLeuValSerLeuProProSerIleAspArgProGlu     81
                      |||
Db   226 GGGCGGCAGCAGACGCCCCGGGACAGTTTCCGCTGCGGACAGACTTTTGGCTC         285

Qy    82 ArgHisValProIleAspPheTyrGlnValLeuGlyAlaGlnThrHisPheLeu          101
         |||||||||:::||
Db   286 AAGGGGTACCGCAATCCCCGCC------------------------TATGAGCTC         346

Qy   102 ThrAspGlyIleArgArgAlaPheGluAlaArgValSerLysProProGlnPheGly      121
         |||||:::||
Db   328 GCGGACGATATTATCGGAACAGATGGGCGGCGGCTGAGCGAGAA------GGGTTT       378

Qy   122 SerAspAspAlaLeuIleLeuSerArgArgArgGlnIleLeuGluThrLeuSer          141
         |||
Db   379 GCAGTGAAAGTCATTTCCGGCGACACCGGCGATTTAACCCAG------CTTGCT         423

Qy   142 AsnProArgSerArgArgGluTyr--AsnGluGlyLeuLeuAspAspProGluGluAlaThr  160
         ::::||||:::||:::
Db   424 TCCCCGCCAAGTGACGGTGGAGATTACGACAAAAAAGGGGATTACCGACATCGAGTGTACACG 483

Qy   161 ValIleThrArgAspVal------                                         165
         |||
Db   484 CCGGACACGGTCGTGGAAAAAATACGGGCCTCACCCCGGAGCAAAATTGTCGACTTGAAAGGA 543

Qy   166 ---------ProTrpAspLysValProGly-                                  166
         :::
Db   544 TTGATGGGCGACAAAATCCGACAACATCCCTGCGGCCGGAAAAAACAGCC            603

Qy   174 LeuCysValLeuGlnLeuGlyLeuGlyGluThrArgGluThr--AsnGluGlyLeuLeuAsp   193
         |||
Db   604 GTCAAGCTGCTCAAGCAGCAACTGGACGGTGGAGATTACGACAAAAAAGGGGATTACCGA   663

Qy   194 LeuLysGluArgLeuProLysSerPheLysGly-Gln                            211
         |||
Db   664 AAAAGGGGAGAAGCTGAAAGAAAATTTGCGCAATACGGGGATTTGCGGCCTT---TTAAGC  720

Qy   212 LeuAlaPheLeuAspValSerArgAspAla------MetAlaLeuAspProProAsp       228
         :::
Db   721 AAACAGCTGGCCGGCTATTTGCCGCAGCGCCCCCGGTTGAGCTGACGCTCGAT---GAC   774

Qy   229 PheIleThrGlyTyrGlyLuPheValGlyLeuAlaLeuLysLeuLeuGlnGluGlyGlyVal   248
         :::
Db   775 ATTGTCTACAAAAGGACGAGAACCCGGGAAAAGTGGTCGCCTTGTTTCAGGAGCTCGGATTC  834

Qy   249 SerSerLeuAlaProLeuArgAlaGlnIleLeuAspGlu                          261
         :::
Db   835 CAGTCGTTTCTGACAAGATGGCCCGTCCAAACGACGAGAGGCGAAAAGCCCTCCGCGGG    894

Qy   262 --------ThrLeuGluGlyIleLeuThrProArgTyrValPheIleLeuGluLeuGlyLeu   277
         :::
Db   895 ATGGATTTTGGGATCCGGACCCGGACGAAATGCTCGGACAAAGCGGCCCTC           954

Qy   278 --------ProLeuGlyAspAspAsnPheTyr-AlaAlaLysArgLeuAsnGlyLeuSerGlyVa  294
         :::
Db   955 GTCGTGGAGGTGGTCCGGACAACTATCACCATGCCCGATTGTCCGGATCGCCT----    1009

Qy   294 1ArgAsnIleLeuTrpSerValGlyValGlyGlyValAlaSer-AlaLeuValGlyLyLeuT   314
         :::
Db  1010 TGGCCAACGAACGCGGCGGGTTTTTCCTGCGCGAGACGGCGGGTTGACGCGGCTC       1056

Qy   314 hrArgGluLysPheMetAsnGluAlaAlaPhe                                 323
         |||:::
Db  1057 GCCGATCCGAAATTTCTCGCTTGGCCTTGGCCGATGAGACGGAGAAAAAACGATGTTTGAT  1116

Qy   324 -------------LeuArgMetThrAlaAlaGluGluGlnVal-                     332
         |||:::
Db  2056 GCCATGGACATTTTCCATGTGAGCGGAAGAAGACGTGACAGCCAACATGCGCCAAGCG     2115
```

```
Db  1117 TCAAAGCGGCGGGCGGCGCCTCGGGGCCTAAAAATGGAAAGGAAATCGGCGGCGGTTC      1176

Qy   347 ---PheGluValTyrGluValAlaIleAlaLeuAlaLeuAlaGlnAlaPheIleGlyLys-   364
         ||||||
Db  1237 GTGGCCGAAAATGCATCAGTACGAGCGGGCGTGCGGATCGGGGTCGTATGGAAAAAGGA    1296

Qy   333 AspLeuPheValAlaThrProSerAsnIleProAlaGluSer-----                  346
         :::||||
Db  1177 GATCCTGTTGCTGGCCGCCTTACTTCGTCGATCCGGCGGGCAGCGGCGGTTGCCGG       1236

Qy   365 ---------LysProHisLeuLeuGlnAspAlaAspLysGlnPheGln-                377
         |||
Db  1297 GCGGAAGCGGACGGGTTCCTGATGAACGACGCCTTGCCGAGCGATCCGCCCGCC        1347

Qy   378 GlnLeuGlnGlnIleAlaLysValMetAlametGluIleIleProAlaMetLeuTyrArgThrArg 397
         :::||||
Db  1348 ------AAGGCGGGCCCCCCATTTGGCGTGCTTGATGGACGAACGCCCCGC----        1401

Qy   398 AsnAsnTrpGlu------IleAspPheGlyLeuGluGlyGlyLeuCysGlyAlaLeuLeuIleGly 416
         :::
Db  1402 AACGAACAAGATCGGCCTGCTGACCGAGCTGGAACAGCCGCCTGGCCGTGGCCAAT        1461

Qy   417 ------------LysValAspGluCysArgMet---TrpLeuGlyLeuAsp-            428
         |||||||
Db  1570 CAAGAGTTCAACATTAACTCGCCG-----------AAACAGCTCGGGACG            1608

Qy   429 SerGluAspSerGlnTyrArgAsnProAlaIleVVlLeValLeuLeuAsnSerAsn        448
         :::||||
Db  1462 ATGGAAATTTACTGGAGTGAAAAGTGGCAACACGAAGCGGCCTTGAACAGATGGGGGGCGAGCTC 1521

Qy   449 ArgAspAspAsnAspAspLeuProGlyLeuCysGlyLysLeuLeuGluThrTrpLeuAlaGly 468
         |||||||
Db  1666 ACTTCAGCCGATCTGCTTGAGAAGCTTCCACCCGCACCATGAAAATCGTCGAA----CAT  1719

Qy   469 ValValPheProArgPheArgAspThrLysLysPheLysLysPheLysGlyTyrTyr       488
         |||||||
Db  1609 GTTTTATTTGACAAGCTCGCAGCTCCCCGGTGTTGAAAAAGGACAAAAACCGGC------TATTCG 1665

Qy   489 AspAspProMetValLeuSerPheTyrLeu--GluArgValGluValValGlnGlySerPro 507
         :::
Db  1777 AAAGTGGTGCACCCCGTGACGGCGCAAAGTGCACACAGTGTTCAAATCAGGCG         1827

Qy   508 LeuAlaAlaAlaThrMetAlaArgIleGlyAlaGlyHisValAlaLeuAlaSerAlaMet    527
         :::
Db  1720 ATTTTTGCATTACCGCCAACTCGGCAGTCGCAGCCGTCAGTCATAACGGTAATATTGAA---  1776

Qy   528 GlnAlaLeuGlnLysLysValPheProSerArgTyrThrArgAspArgAsnSerAlaGluProLys 547
         :::
Db  1828 --TTGACGCAAACCGGCGCCTTCAGCTCACGTCGGAACCGGAATTTGCAAAACAATTCCGATT 1884

Qy   548 AspAspValGlnGluThr------ValPheSerValAspProValGlyAsnValGlyArg    565
         :::
Db  1945 ATCTTTGCGGCCGGACTATTCGGCAAAATCGAGTCGGCGGTCGCCATAATCGGCGG       2001

Qy   566 AspGlyValGluProGlyValPheIleAlaGluAlaValArgProSerGlu-            581
         |||||||
Db  1885 CGGCCTTGAGGGAAGGCGGGGAAAATCCGGCGCTTCGGTGCCGGCGGACTGGCTC        1944

Qy   582 -------------AsnPheGluThrAsnAspTyrAlaIleAlaArgAlaAlaGlyValSerGluSer 597
         :::
Db  2002 --GATGACAAATTTGATTGAAGGGTTCCGGCGGTTGACAATCCATACGAAAACA          2055

Qy   598 SerValAspGluThrThrValGlu------                                   605
         :::
Db  2056 ---MetSerValAlaAspMetLeuLysGlu---------AlaSerValLysIleLeuVala   621

Qy   606 ---MetSerValAlaAspMetLeuLysGlu--------AlaSerValLysIleLeuVala    621
         |||
Db  2056 GCCATGGACATTTTCCATGTGAGCGGAAGAAGACGTGACAGCCAACATGCGCCAAGCG     2115

Qy   622 AlaGlyValAlaIleGlyTyrLeuIleSerLeuPheSerGlnLysTyrPheLeuLysSerSer  641
         |||:::::
```

```
Db   2116 AAGGCCGTCAAATTTTGGCATCGTTGTACGGCGATTAGTGAT---TACGGTCTGGGCCGAAAAC 2172

Qy    642 SerSerPheGlnArgLysAspMetValSerSerMetGluSerAspValAlaThrIleGly 661
               ||||||||||:::     :::|||              |||||:::
Db   2173 TTGAACATTACGCGCAAAGAACGGGCTGAATTTATTGAGCGGATATTTTGCCAGTTTTCCA 2232

Qy    662 SerValArgAlaAspAspSerGluAlaLeuProArgMetAspAlaArgThrAlaGluAsn 681
               ||:::                                       :::|||
Db   2233 GGTGTAAAG--------------------------------------CAATATATGGACAAC 2256

Qy    682 IleValSerLysTrpGlnLysIleLysSerLeuAlaPheGlyProAspHisArgIleGlu 701
               |||||||     :::                               |||||||
Db   2257 ATTGTGCAAGAA--GCGAAACAAAAAGGGTATGTGACGACGCTGCATCGGCGCCCGC 2313

Qy    702 MetLeuProGluValLeuAspGlyArgMet---LeuLysIleTrpThrAsppArgAlaAla 720
               ||||||||||                :::||||      :::|||        |||
Db   2314 TATTTGCCCGATATTACAAGCCGCAACTTCAAACGTCCGCAGCTTCGCGAGCGGACGGCG 2373

Qy    721 ---GluThrAlaGlnLeuGlyTyrLeuValTyrAspTyrThrLeuLeuLysLeuSerValAsp 739
               |||                :::        |||:::        |||
Db   2374 ATGAACACACCGGATCCAAAGGGAGTGCCGCTGAT---ATTATTAAAAAAGCCGGATGATCGGAT 2430

Qy    740 ---SerValThrValSerAlaAspGlyThrArgAla--------------------------- 750
               |||||||       :::   |||
Db   2431 CTAAGCGGTGAGGCTGCGCGGAGAACCGGCCCGGGCCGCTGTTGCTGCAAGTGCATGAC 2490

Qy    751 -----LeuValGluAlaThrLeuGluGluSerAlaCysLeuSerAspLeuValHisPro 768
               :::::||||||                 ||||||||||        |||
Db   2491 GAACTCATTTTCGAGGGCGCCCGAAAGAGGAAATCGAGCGGGCTGTGCGCCCTCGTTT---CCA 2547

Qy    769 Glu 769
          |||
Db   2548 GAG 2550
```